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Sir:

Transmitted herewith for filing is the patent application of:

Inventors: Markus Pompejus *et al.*For: "*Corynebacterium Glutamicum* Genes Encoding Stress, Resistance, and Tolerance Proteins"

Enclosed are:

- ☒ 62 pages of specification, 5 pages of claims and 1 page of abstract;
- ☒ 4 pages of Table 1;
- ☒ 16 pages of Table 2;
- ☒ 6 pages of Table 3;
- ☒ 8 pages of Table 4;
- ☒ 59 pages of Appendix A;
- ☒ 19 pages of Appendix B;
- ☒ 389 pages of Sequence Listing;
- ☒ Diskette Containing Sequence Listing;
- ☒ Transmittal Letter for Diskette Containing Sequence Listing;
- ☒ An *unexecuted* Declaration, Petition and Power of Attorney;
- ☒ A pre-paid acknowledgment postcard.

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Address all future communications (May only be completed by applicant, or attorney or agent of record) to **Elizabeth A. Hanley, Esq. at Customer Number: 000959** whose address is:

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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING STRESS,
RESISTANCE AND TOLERANCE PROTEINS**

Related Applications

- 5 This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial No. 60/142692, filed July 1, 1999, and also to U.S. Provisional Patent Application Serial No. 60/151214, filed August 27, 1999. This application also claims priority to German Patent Application No. 19930429.7, filed July 1, 1999, German Patent Application No. 19931413.6, filed July 8, 1999, German Patent Application No. 19931457.8, filed July 8, 1999, German Patent Application No. 19931541.8, filed July 8, 1999, German Patent Application No. 19932209.0, filed July 9, 1999, German Patent Application No. 19932230.9, filed July 9, 1999, German Patent Application No. 19932914.1, filed July 14, 1999, German Patent Application No. 19940764.9, filed August 27, 1999, and 10 German Patent Application No. 19941382.7, filed August 31, 1999. The entire contents of all of the aforementioned applications are hereby expressly incorporated herein in their entirety by this reference.

Background of the Invention

- 20 Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic 25 compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through large-scale culture of bacteria developed to produce and secrete large quantities of a particular desired molecule. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have 30 been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

- 35 The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C.*

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glutamicum or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as stress, resistance and tolerance (SRT) proteins.

5 *C. glutamicum* is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The SRT nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by
10 fermentation processes. Modulation of the expression of the SRT nucleic acids of the invention, or modification of the sequence of the SRT nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

15 The SRT nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or
20 mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of
25 significant clinical relevance.

 The SRT nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

30 The SRT proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, permitting *C. glutamicum* to survive in a setting which is either chemically or environmentally hazardous to this microorganism. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic
35 manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-

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2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals, through the ability of these proteins to permit growth and multiplication of *C. glutamicum* (and also continuous production of one or more fine chemicals) under circumstances which would normally impede growth of the organism, such as those conditions frequently encountered during large-scale fermentative growth. For example, by overexpressing or engineering a heat-shock induced protease molecule such that it is optimized in activity, one may increase the ability of the bacterium to degrade incorrectly folded proteins when the bacterium is challenged with high temperatures. By having fewer misfolded (and possibly misregulated or nonfunctional) proteins to interfere with normal reaction mechanisms in the cell, the cell is increased in its ability to function normally in such a culture, which should in turn provide increased viability. This overall increase in number of cells having greater viability and activity in the culture should also result in an increase in yield, production, and/or efficiency of production of one or more desired fine chemicals, due at least to the relatively greater number of cells producing these chemicals in the culture.

This invention provides novel SRT nucleic acid molecules which encode SRT proteins which are capable of, for example, permitting *C. glutamicum* to survive in a setting which is either chemically or environmentally hazardous to this microorganism. Nucleic acid molecules encoding an SRT protein are referred to herein as SRT nucleic acid molecules. In a preferred embodiment, the SRT protein participates in metabolic pathways permitting *C. glutamicum* to survive in a setting which is either chemically or environmentally hazardous to this microorganism. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (e.g., cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an SRT protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of SRT-encoding nucleic acid (e.g., DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in Appendix A or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the

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amino acid sequences set forth in Appendix B. The preferred SRT proteins of the present invention also preferably possess at least one of the SRT activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or
5 portion thereof wherein the protein or portion thereof includes an amino acid sequence
which is sufficiently homologous to an amino acid sequence of Appendix B, *e.g.*,
sufficiently homologous to an amino acid sequence of Appendix B such that the protein
or portion thereof maintains an SRT activity. Preferably, the protein or portion thereof
10 encoded by the nucleic acid molecule maintains the ability to increase the survival of *C.*
glutamicum in a setting which is either chemically or environmentally hazardous to this
microorganism. In one embodiment, the protein encoded by the nucleic acid molecule
is at least about 50%, preferably at least about 60%, and more preferably at least about
70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or
15 more homologous to an amino acid sequence of Appendix B (*e.g.*, an entire amino acid
sequence selected from those sequences set forth in Appendix B). In another preferred
embodiment, the protein is a full length *C. glutamicum* protein which is substantially
homologous to an entire amino acid sequence of Appendix B (encoded by an open
reading frame shown in Appendix A).

In another preferred embodiment, the isolated nucleic acid molecule is derived
20 from *C. glutamicum* and encodes a protein (*e.g.*, an SRT fusion protein) which includes
a biologically active domain which is at least about 50% or more homologous to one of
the amino acid sequences of Appendix B and has the ability to increase the survival of
C. glutamicum in a setting which is either chemically or environmentally hazardous to
this microorganism, or possesses one or more of the activities set forth in Table 1, and
25 which also includes heterologous nucleic acid sequences encoding a heterologous
polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15
nucleotides in length and hybridizes under stringent conditions to a nucleic acid
molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated
30 nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More
preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* SRT
protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression
vectors, containing the nucleic acid molecules of the invention, and host cells into which
35 such vectors have been introduced. In one embodiment, such a host cell is used to
produce an SRT protein by culturing the host cell in a suitable medium. The SRT
protein can be then isolated from the medium or the host cell.

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Yet another aspect of the invention pertains to a genetically altered microorganism in which an SRT gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by the introduction of a nucleic acid molecule of the invention encoding wild-type or mutated SRT sequence as a transgene. In another embodiment, an endogenous SRT gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered SRT gene. In another embodiment, an endogenous or introduced SRT gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SRT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of a SRT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SRT gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated SRT protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated SRT protein or portion thereof possesses the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism. In another preferred embodiment, the isolated SRT protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism.

The invention also provides an isolated preparation of an SRT protein. In preferred embodiments, the SRT protein comprises an amino acid sequence of Appendix B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more

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preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of Appendix B. In other embodiments, the isolated SRT protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to improve the survival rate of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated SRT protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of SRT proteins also have one or more of the SRT bioactivities described herein.

The SRT polypeptide, or a biologically active portion thereof, can be operatively linked to a non-SRT polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the SRT protein alone. In other preferred embodiments, this fusion protein results in increased yields, production, and/or efficiency of production of a desired fine chemical from *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates the production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an SRT protein, either by interacting with the protein itself or a substrate or binding partner of the SRT protein, or by modulating the transcription or translation of an SRT nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an SRT nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an SRT nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates SRT protein activity or SRT nucleic acid expression such that a

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cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated in resistance to one or more toxic chemicals or in resistance to one or more environmental stresses, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates SRT protein activity can be an agent which stimulates SRT protein activity or SRT nucleic acid expression. Examples of agents which stimulate SRT protein activity or SRT nucleic acid expression include small molecules, active SRT proteins, and nucleic acids encoding SRT proteins that have been introduced into the cell. Examples of agents which inhibit SRT activity or expression include small molecules, and antisense SRT nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant SRT gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides SRT nucleic acid and protein molecules which are involved in the survival of *C. glutamicum* upon exposure of this microorganism to chemical or environmental hazards. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, since these SRT proteins provide a means for continued growth and multiplication of *C. glutamicum* in the presence of toxic chemicals or hazardous environmental conditions, such as may be encountered during large-scale fermentative growth. By increasing the growth rate or at least maintaining normal growth in the face of poor, if not toxic, conditions, one may increase the yield, production, and/or efficiency of production of one or more fine chemicals from such a culture, at least due to the relatively greater number of cells producing the fine chemical in the culture. Aspects of the invention are further explicated below.

I. Fine Chemicals

- The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in *Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) *Chemicals by Fermentation*, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. Amino Acid Metabolism and Uses

- Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ullmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. *Biochemistry*, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways

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to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

- 5 Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly
10 used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-
15 methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others
20 described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

- The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine
25 are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both
30 cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step
35 biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction

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catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

20 *B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses*

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms, such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such

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molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCs Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (*e.g.*, pyridoxine, pyridoxamine, pyridoxal-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β-alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β-alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthanol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α-ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the

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metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system.

- 5 The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

- 10 The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

- 20 Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

- 30 Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the

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development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates

5 in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-

10 612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide

15 biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher

20 animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so

25 their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate

30 deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α , α -1,1 linkage. It is

35 commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S.

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- Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Resistance to Damage from Chemicals, Environmental Stress, and Antibiotics

- Production of fine chemicals is typically performed by large-scale culture of bacteria developed to produce and secrete large quantities of these molecules. However, this type of large-scale fermentation results in the subjection of the microorganisms to stresses of various kinds. These stresses include environmental stress and chemical stress.

A. Resistance to Environmental Stress

- Examples of environmental stresses typically encountered in large-scale fermentative culture include mechanical stress, heat stress, stress due to limited oxygen, stress due to oxygen radicals, pH stress, and osmotic stress. The stirring mechanism used in most large-scale fermentors to ensure aeration of the culture produces heat, thus increasing the temperature of the culture. Increases in temperature induce the well-characterized heat shock response, in which a set of proteins are expressed which not only aid in the survival of the bacterium in the face of high temperatures, but also increase survival in response to a number of other environmental stresses (see Neidhardt, F.C., *et al.*, eds. (1996) *E. coli* and *Salmonella*. ASM Press: Washington, D.C., p. 1382-1399; Wosten, M. M. (1998) *FEMS Microbiology Reviews* 22(3): 127-50; Bahl, H. *et al.* (1995) *FEMS Microbiology Reviews* 17(3): 341-348; Zimmerman, J.L., Cohill, P.R. (1991) *New Biologist* 3(7): 641-650; Samali, A., and Orrenius, S. (1998) *Cell. Stress Chaperones* 3(4): 228-236, and references contained therein from each of these citations). Regulation of the heat shock response in bacteria is facilitated by specific sigma factors and other cellular regulators of gene expression (Hecker, M., Volker, U (1998). *Molecular Microbiology* 29(5): 1129-1136). One of the largest problems that the cell encounters when exposed to high temperature is that protein folding is impaired; nascent proteins have sufficient kinetic energy in high temperature circumstances that it is difficult for the growing polypeptide chain to remain in a stable conformation long enough to fold properly. Thus, two of the key types of proteins expressed during the heat shock response consist of chaperones (proteins which assist in the folding or unfolding of other proteins – see, *e.g.*, Fink, A.L. (1999) *Physiol. Rev.* 79(2): 425-449), and proteases, which can destroy any improperly folded proteins.

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Examples of chaperones expressed during the heat shock response include GroEL and DNAK; proteases known to be expressed during this cellular reaction to heat shock include Lon, FtsH, and ClpB.

Other environmental stresses besides heat may also provoke a stress response.

- 5 Though the fermentor stirring process is meant to introduce oxygen into the culture, oxygen may remain in limited supply, particularly when the culture is advanced in growth and the oxygen needs of the culture are thereby increased; an insufficient supply of oxygen is another stress for the microorganism. Cells in fermentor cultures are also subjected to a number of osmotic stresses, particularly when nutrients are added to the
- 10 culture, resulting in a high extracellular and low intracellular concentration of these molecules. Further, the large quantities of the desired molecules produced by these organisms in culture may contribute to osmotic stress of the bacteria. Lastly, aerobic metabolism such as that used by *C. glutamicum* results in carbon dioxide as a waste product; secretion of this molecule may acidify the culture medium due to conversion of
- 15 this molecule to carboxylic acid. Thus, bacteria in culture are also frequently subjected to acidic pH stress. The converse may also be true – when high levels of basic waste molecules such as ammonium are present in the culture medium, the bacteria in culture may be subjected to basic pH stress as well.

- To combat such environmental stresses, bacteria have elegant gene systems
- 20 which are expressed upon exposure to one or more stresses, such as the aforementioned heat shock system. Genes expressed in response to osmotic stress, for example, encode proteins capable of transporting or synthesizing compatible solutes such that osmotic intake or export of a particular molecule is slowed to manageable levels. Other examples of stress-induced bacterial proteins are those involved in trehalose biosynthesis, those
- 25 encoding enzymes involved in ppGpp metabolism, those involved in signal transduction, particularly those encoding two-component systems which are sensitive to osmotic pressure, and those encoding transcription factors which are responsive to a variety of stress factors (e.g., RssB analogues and/or sigma factors). Many other such genes and their protein products are known in the art.

30

B. Resistance to Chemical Stress

- Aside from environmental stresses, cells may also experience a number of chemical stresses. These may fall into two categories. The first are natural waste products of metabolism and other cellular processes which are secreted by the cell to the
- 35 surrounding medium. The second are chemicals present in the extracellular medium which do not originate from the cell. Generally, when cells excrete toxic waste products from the concentrated intracellular cytoplasm into the relatively much more dilute

extracellular medium, these products dissipate such that extracellular levels of the possibly toxic compound are quite low. However, in large-scale fermentative culture of the bacterium, this may not be the case: so many bacteria are grown in a relatively small environment and at such a high metabolic rate that waste products may accumulate in the medium to nearly toxic levels. Examples of such wastes are carbon dioxide, metal ions, and reactive oxygen species such as hydrogen peroxide. These compounds may interfere with the activity or structure of cell surface molecules, or may re-enter the cell, where they can seriously damage proteins and nucleic acids alike. Certain other chemicals hazardous to the normal functioning of cells may be naturally found in the extracellular medium. For example, metal ions such as mercury, cadmium, nickel or copper are frequently found in water sources, and may form tight complexes with cellular enzymes which prevent the normal functioning of these proteins.

C. Resistance to Antibiotics

Bacteriocidal proteins or antibiotics, may also be found in the extracellular milieu, either through the intervention of the researcher, or as a natural product from another organism, utilized to gain a competitive advantage. Microorganisms have several art-known mechanisms to protect themselves against antimicrobial chemicals. Degradation, modification, and export of compounds toxic to the cell are common methods by which microorganisms eliminate or detoxify antibiotics. Cytoplasmic 'efflux-pumps' are known in several prokaryotes and show similarities to the so-called 'multidrug resistance' proteins from higher eukaryotes (Neyfakh, A. A. , *et al.* (1991) *Proc. Natl. Acad. Sci. USA* 88: 4781-4785). Examples of such proteins include *emrAB* from *E. coli* (Lomovskaya, O. and K. Lewis (1992) *Proc. Natl. Acad. Sci. USA* 89: 8938-8942), *lmrB* from *B. subtilis* (Kumano, M. *et al.* (1997) *Microbiology* 143: 2775-2782), *smr* from *S. aureus* (Grinius, L.G. *et al.* (1992) *Plasmid* 27: 119-129) or *cmr* from *C. glutamicum* (Kaidoh, K. *et al.* (1997) *Micro. Drug Resist.* 3: 345-350). *C. glutamicum* itself is non-pathogenic, in contrast to several other members of the genus *Corynebacterium* , such as *C. diphtheriae* or *C. pseudotuberculosis*. Several pathogenic *Corynebacteria* are known to have multiple resistances against a variety of antibiotics, such as *C. jeikeium* and *C. urealyticum* (Soriano, F. *et al.* (1995) *Antimicrob. Agents Chemother.* 39: 208-214).

Lincosamides are recognized as effective antibiotics against *Corynebacterium* species (Soriano, F. *et al.* (1995) *Antimicrob. Agents Chemother.* 39: 208-214). An unexpected result of the present invention was the identification of a gene encoding a lincosamide-resistance protein (in particular, a lincomycin-resistance protein). The LMRB protein from *C. glutamicum* shows 40% homology to the product of the *lmrB*

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- gene from *B. subtilis* (see Genbank accession no. AL009126), as calculated using version 1.7 of the program CLUSTALW (Thompson, J.D., Higgins, D.G., Gibson, T. J. (1994) *Nucl. Acids Res.* 22: 4673-4680) using standard parameters (PAIRWISE ALIGNMENT PARAMETERS: slow/accurate alignments: Gap Open Penalty = 10.00, 5 Gap Extension Penalty = 0.10, Protein weight matrix = BLOSUM 30, DNA weight matrix = IUB, Fast/Approximate alignments: Gap penalty = 3, K-tuple (word) size = 1, No. of top diagonals = 5, Window size = 5, Toggle Slow/Fast pairwise alignments = slow. Multiple alignment parameters: Gap Opening Penalty = 10.00, Gap Extension Penalty = 0.05, Delay divergent sequences = 40%, DNA transitions weight = 0.50, 10 Protein weight matrix = BLOSUM series, DNA weight matrix = IUB, Use negative matrix = OFF).

- Environmental stress, chemical stress, and antibiotic or other antimicrobial stress may influence the behavior of the microorganisms during fermentor culture, and may have an impact on the production of the desired compound from these organisms. 15 For example, osmotic stress of a microorganism may cause inappropriate or inappropriately rapid uptake of one or more compounds which can ultimately lead to cellular damage or death due to osmotic shock. Similarly, chemicals present in the culture, either exogenously added (*e.g.*, antimicrobial compounds intended to eliminate unwanted microbes) or generated by the bacteria themselves (*e.g.*, waste compounds 20 such as heavy metals or oxygen radicals, or even antimicrobial compounds) may result in inhibition of fine chemical production or even death of the organism. The genes of the invention encode *C. glutamicum* proteins which act to prevent cell damage or death, by specifically counteracting the source or effect of the environmental or chemical stress.

25

III. Elements and Methods of the Invention

- The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as SRT nucleic acid and protein molecules, which increase the ability of *C. glutamicum* to survive in chemically or environmentally hazardous 30 settings. In one embodiment, the SRT molecules function to confer resistance to one or more environmental or chemical stresses to *C. glutamicum*. In a preferred embodiment, the activity of the SRT molecules of the present invention has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the SRT molecules of the invention are modulated in activity, such that the 35 yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum* is also modulated.

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The language, "SRT protein" or "SRT polypeptide" includes proteins which participate in the resistance of *C. glutamicum* to one or more environmental or chemical stresses. Examples of SRT proteins include those encoded by the SRT genes set forth in Table 1 and Appendix A. The terms "SRT gene" or "SRT nucleic acid sequence" include nucleic acid sequences encoding an SRT protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of SRT genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (e.g., kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (i.e., fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (e.g., the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound. The terms "resistance" and "tolerance" are art-known and include the ability of a cell to not be affected by exposure to a chemical or an environment which would otherwise be detrimental to the normal functioning of these organisms. The terms "stress" or "hazard" include factors which are detrimental to the normal functioning of cells such as *C. glutamicum*. Examples of stresses include "chemical stress", in which a cell is exposed to one or more chemicals which are detrimental to the cell, and "environmental stress" where a cell is exposed to an environmental condition outside of those to which it is adapted. Chemical stresses may be either natural metabolic waste products such as, but not limited to reactive oxygen species or carbon dioxide, or

chemicals otherwise present in the environment, including, but not limited to heavy metal ions or bacteriocidal proteins such as antibiotics. Environmental stresses may be, but are not limited to temperatures outside of the normal range, suboptimal oxygen availability, osmotic pressures, or extremes of pH, for example.

- 5 In another embodiment, the SRT molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or more of the SRT proteins of the invention may be manipulated such that its function is modulated. The alteration of activity of stress response, resistance or tolerance genes
- 10 such that the cell is increased in tolerance to one or more stresses may improve the ability of that cell to grow and multiply in the relatively stressful conditions of large-scale fermentor culture. For example, by overexpressing or engineering a heat-shock induced chaperone molecule such that it is optimized in activity, one may increase the ability of the bacterium to correctly fold proteins in the face of nonoptimal temperature
- 15 conditions. By having fewer misfolded (and possibly misregulated or nonfunctional) proteins, the cell is increased in its ability to function normally in such a culture, which should in turn provide increased viability. This overall increase in number of cells having greater viability and activity in the culture should also result in an increase in the yield, production, and/or efficiency of production of one or more desired fine chemicals,
- 20 due at least to the relatively greater number of cells producing these chemicals in the culture.

- The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the
- 25 isolated *C. glutamicum* SRT DNAs and the predicted amino acid sequences of the *C. glutamicum* SRT proteins are shown in Appendices A and B, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode chemical and environmental stress, resistance, and tolerance proteins.

- 30 The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B. As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, e.g., the entire selected amino acid sequence. A protein
- 35 which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at

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least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence. Ranges and identity values intermediate to the above-recited values, (e.g., 75%-80% identical, 85-87% identical, 91-92% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included.

The SRT proteins or biologically active portions or fragments thereof of the invention can confer resistance or tolerance to one or more chemical or environmental stresses, or may have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode SRT polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of SRT-encoding nucleic acid (e.g., SRT DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated SRT nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g., a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

5 A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* SRT DNA can be isolated from a *C. glutamicum* library

10 using all or portion of one of the sequences of Appendix A as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsch, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences

15 of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of Appendix A). For example, mRNA can be isolated from normal endothelial cells (*e.g.*,

20 by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be

25 designed based upon one of the nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore,

oligonucleotides corresponding to an SRT nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of Appendix A correspond to the *Corynebacterium glutamicum* SRT DNAs of the

30 invention. This DNA comprises sequences encoding SRT proteins (*i.e.*, the "coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix A.

35 For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA, RXN, or RXS number having the designation "RXA", "RXN", or "RXS" followed by 5 digits (*i.e.*,

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RXA01524, RXN00493, or RXS01027). Each of these sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the sequences in Appendix A", then, refers to any of the sequences in Appendix A, which may be distinguished by their differing RXA, RXN, or RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA, RXN, or RXS designations as Appendix A, such that they can be readily correlated. For example, the amino acid sequence in Appendix B designated RXA01524 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA01524 in Appendix A, the amino acid sequence in Appendix B designated RXN00034 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXN00034 in Appendix A, and the amino acid sequence in Appendix B designated RXS00568 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXS00568 in Appendix A. Each of the RXA, RXN, and RXS nucleotide and amino acid sequences of the invention has also been assigned a SEQ ID NO, as indicated in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, or RXS designation. For example, SEQ ID NO:7, designated, as indicated on Table 1, as "F RXA00498", is an F-designated gene, as are SEQ ID NOs: 25, 33, and 37 (designated on Table 1 as "F RXA01345", "F RXA02543", and "F RXA02282", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in Appendix A is one which is sufficiently complementary to one of the nucleotide sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown in Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an SRT protein. The nucleotide sequences determined from the cloning of the SRT genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning SRT homologues in other cell types and organisms, as well as SRT homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of Appendix A can be used in PCR reactions to clone SRT homologues. Probes based on the SRT nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, e.g. the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an SRT protein, such as by measuring a level of an SRT-encoding nucleic acid in a sample of cells, e.g., detecting SRT mRNA levels or determining whether a genomic SRT gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to confer resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (e.g., an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix B such that the protein or portion thereof is capable of participating in the resistance of *C. glutamicum* to one or more chemical or environmental stresses. Protein members of such metabolic pathways, as described herein, function to increase the resistance or tolerance of *C. glutamicum* to one or more environmental or chemical hazards or stresses. Examples of such activities are also described herein. Thus, "the function of an SRT protein" contributes to the overall resistance of *C. glutamicum* to elements of its surroundings which may impede its normal growth or functioning, and/or contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of SRT protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B. Ranges and identity values intermediate to the above-recited values, (e.g., 75%-80% identical, 85-87% identical, or 91-92% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included.

Portions of proteins encoded by the SRT nucleic acid molecules of the invention are preferably biologically active portions of one of the SRT proteins. As used herein, the term "biologically active portion of an SRT protein" is intended to include a portion, e.g., a domain/motif, of an SRT protein that is capable of imparting resistance or tolerance to one or more environmental or chemical stresses or hazards, or has an activity as set forth in Table 1. To determine whether an SRT protein or a biologically active portion thereof can increase the resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses or hazards, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an SRT protein can be prepared by isolating a portion of one of the sequences in Appendix B, expressing the encoded portion of the SRT protein or peptide (e.g., by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SRT protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy of the genetic code and thus encode the same SRT protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (e.g., a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00084 (SEQ ID NO:189), a nucleotide sequence which is greater than and/or at least 56% identical to the nucleotide sequence designated RXA00605 (SEQ ID NO:11), and a nucleotide sequence which is greater than and/or at least 50% identical to the nucleotide sequence designated RXA00886 (SEQ ID NO:39). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (e.g., at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or

90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* SRT nucleotide sequences shown in Appendix A, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of SRT proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the SRT gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an SRT protein, preferably a *C. glutamicum* SRT protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the SRT gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in SRT that are the result of natural variation and that do not alter the functional activity of SRT proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* SRT DNA of the invention can be isolated based on their homology to the *C. glutamicum* SRT nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art in the art and can be found in Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having

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a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* SRT protein.

- In addition to naturally-occurring variants of the SRT sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded SRT protein, without altering the functional ability of the SRT protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the SRT proteins (Appendix B) without altering the activity of said SRT protein, whereas an "essential" amino acid residue is required for SRT protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved in the domain having SRT activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SRT activity.

- Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding SRT proteins that contain changes in amino acid residues that are not essential for SRT activity. Such SRT proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the SRT activities described herein.
- In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Appendix B and is capable of increasing the resistance or tolerance of *C. glutamicum* to one or more environmental or chemical stresses, or has one or more of the activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B, more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

- To determine the percent homology of two amino acid sequences (*e.g.*, one of the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of

the sequence selected from Appendix B), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences

5 (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an SRT protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that one or more amino acid substitutions, additions or deletions are introduced into the

10 encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a

15 similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine,

20 proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an SRT protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly

25 along all or part of an SRT coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an SRT activity described herein to identify mutants that retain SRT activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of

30 the Exemplification).

In addition to the nucleic acid molecules encoding SRT proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*,

35 complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be

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complementary to an entire SRT coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an SRT protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (e.g., the entire coding region of SEQ ID NO.: 120 (RXA00600) comprises nucleotides 1 to 1098). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding SRT. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding SRT disclosed herein (e.g., the sequences set forth in Appendix A), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SRT mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of SRT mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SRT mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-

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amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an SRT protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave SRT mRNA transcripts to thereby inhibit translation of SRT mRNA. A ribozyme having specificity for an SRT-encoding nucleic acid can be designed based upon the nucleotide sequence of an SRT cDNA disclosed herein (*i.e.*, SEQ ID NO:119 (RXA00600 in Appendix A)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an SRT-encoding mRNA.

See, e.g., Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, SRT mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

- 5 Alternatively, SRT gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an SRT nucleotide sequence (e.g., an SRT promoter and/or enhancers) to form triple helical structures that prevent transcription of an SRT gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-10 36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

- Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an SRT protein (or a portion thereof). As
15 used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of
20 autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to
25 which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors,
30 such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

- The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory
35 sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of

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- interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells.
- Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI^q*-, *T7*-, *T5*-, *T3*-, *gal*-, *trc*-, *ara*-, *SP6*-, *amy*-, *SPO2*-, λ -*P_R*- or λ *P_L*-, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as *ADC1*, *MF α* , *AC*-, *P-60*, *CYC1*, *GAPDH*, *TEF*, *tp28*, *ADH*, promoters from plants such as *CaMV/35S*, *SSU*, *OCS*, *lib4*, *usp*, *STLS1*, *B33*, *nos* or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, SRT proteins, mutant forms of SRT proteins, fusion proteins, etc.).

- The recombinant expression vectors of the invention can be designed for expression of SRT proteins in prokaryotic or eukaryotic cells. For example, SRT genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells.
- Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the

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recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the SRT protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant SRT protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming

Streptomyces, while plasmids pUB110, pC194, or pBD214 are suited for transformation of Bacillus species. Several plasmids of use in the transfer of genetic information into Corynebacterium include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York ISBN 0 444 904018).

- 5 One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an
- 10 expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

- In another embodiment, the SRT protein expression vector is a yeast expression
- 15 vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (ISBN 0 444 904018).
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- 25 Alternatively, the SRT proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

- 30 In another embodiment, the SRT proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant*
- 35 *Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+,

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pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsch, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campe and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to SRT mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which

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direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an SRT protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA)) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*, 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred

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selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an SRT protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an SRT gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the SRT gene.

Preferably, this SRT gene is a *Corynebacterium glutamicum* SRT gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous SRT gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous SRT gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous SRT protein). In the homologous recombination vector, the altered portion of the SRT gene is flanked at its 5' and 3' ends by additional nucleic acid of the SRT gene to allow for homologous recombination to occur between the exogenous SRT gene carried by the vector and an endogenous SRT gene in a microorganism. The additional flanking SRT nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced SRT gene has homologously recombined with the endogenous SRT gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an SRT gene on a vector placing it under control of the lac operon permits expression of the SRT gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous SRT gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced SRT gene in a host cell has been altered by one or more point mutations,

deletions, or inversions, but still encodes a functional SRT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SRT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SRT gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described SRT gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an SRT protein. Accordingly, the invention further provides methods for producing SRT proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an SRT protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SRT protein) in a suitable medium until SRT protein is produced. In another embodiment, the method further comprises isolating SRT proteins from the medium or the host cell.

C. Isolated SRT Proteins

Another aspect of the invention pertains to isolated SRT proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of SRT protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of SRT protein having less than about 30% (by dry weight) of non-SRT protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-SRT protein, still more preferably less than about 10% of non-SRT protein, and most preferably less than about 5% non-SRT protein. When the SRT protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SRT protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the

protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of SRT protein having less than about 30% (by dry weight) of chemical precursors or non-SRT chemicals, more preferably less than about 20% chemical precursors or non-SRT chemicals, still more preferably less than about 10% chemical precursors or non-SRT chemicals, and most preferably less than about 5% chemical precursors or non-SRT chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the SRT protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* SRT protein in a microorganism such as *C. glutamicum*.

An isolated SRT protein or a portion thereof of the invention can contribute to the resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses or hazards, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to mediate the resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses or hazards. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an SRT protein of the invention has an amino acid sequence shown in Appendix B. In yet another preferred embodiment, the SRT protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still another preferred embodiment, the SRT protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred SRT proteins of the present invention also preferably possess at least one of the SRT activities described herein. For example, a preferred SRT protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a

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nucleotide sequence of Appendix A, and which can increase the resistance or tolerance of *C. glutamicum* to one or more environmental or chemical stresses, or which has one or more of the activities set forth in Table 1.

- In other embodiments, the SRT protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of the sequences of Appendix B yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the SRT protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B and which has at least one of the SRT activities described herein. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B.

- Biologically active portions of an SRT protein include peptides comprising amino acid sequences derived from the amino acid sequence of an SRT protein, e.g., an amino acid sequence shown in Appendix B or the amino acid sequence of a protein homologous to an SRT protein, which include fewer amino acids than a full length SRT protein or the full length protein which is homologous to an SRT protein, and exhibit at least one activity of an SRT protein. Typically, biologically active portions (peptides, e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an SRT protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an SRT protein include one or more selected domains/motifs or portions thereof having biological activity.

- SRT proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as

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described above) and the SRT protein is expressed in the host cell. The SRT protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an SRT protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native SRT protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-SRT antibody, which can be produced by standard techniques utilizing an SRT protein or fragment thereof of this invention.

The invention also provides SRT chimeric or fusion proteins. As used herein, an SRT "chimeric protein" or "fusion protein" comprises an SRT polypeptide operatively linked to a non-SRT polypeptide. An "SRT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to SRT, whereas a "non-SRT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the SRT protein, *e.g.*, a protein which is different from the SRT protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the SRT polypeptide and the non-SRT polypeptide are fused in-frame to each other. The non-SRT polypeptide can be fused to the N-terminus or C-terminus of the SRT polypeptide. For example, in one embodiment the fusion protein is a GST-SRT fusion protein in which the SRT sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant SRT proteins. In another embodiment, the fusion protein is an SRT protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an SRT protein can be increased through use of a heterologous signal sequence.

Preferably, an SRT chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially

available that already encode a fusion moiety (e.g., a GST polypeptide). An SRT-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the SRT protein.

Homologues of the SRT protein can be generated by mutagenesis, e.g., discrete point mutation or truncation of the SRT protein. As used herein, the term "homologue" refers to a variant form of the SRT protein which acts as an agonist or antagonist of the activity of the SRT protein. An agonist of the SRT protein can retain substantially the same, or a subset, of the biological activities of the SRT protein. An antagonist of the SRT protein can inhibit one or more of the activities of the naturally occurring form of the SRT protein, by, for example, competitively binding to a downstream or upstream member of the SRT system which includes the SRT protein. Thus, the *C. glutamicum* SRT protein and homologues thereof of the present invention may increase the tolerance or resistance of *C. glutamicum* to one or more chemical or environmental stresses.

In an alternative embodiment, homologues of the SRT protein can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the SRT protein for SRT protein agonist or antagonist activity. In one embodiment, a variegated library of SRT variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of SRT variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SRT sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of SRT sequences therein. There are a variety of methods which can be used to produce libraries of potential SRT homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SRT sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477).

In addition, libraries of fragments of the SRT protein coding can be used to generate a variegated population of SRT fragments for screening and subsequent selection of homologues of an SRT protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an SRT coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to

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form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the SRT protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SRT homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SRT homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated SRT library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of SRT protein regions required for function; modulation of an SRT protein activity; modulation of the activity of an SRT pathway; and modulation of cellular production of a desired compound, such as a fine chemical.

The SRT nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms

under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.

Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

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The SRT nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The resistance processes in which the molecules of the invention participate are utilized by a wide variety of cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

The genes of the invention, *e.g.*, the gene encoding LMRB (SEQ ID NO:1) or other gene of the invention encoding a chemical or environmental resistance or tolerance protein (*e.g.*, resistance against one or more antibiotics), may be used as genetic markers for the genetic transformation of (*e.g.*, the transfer of additional genes into or disruption of preexisting genes of) organisms such as *C. glutamicum* or other bacterial species. Use of these nucleic acid molecules permits efficient selection of organisms which have incorporated a given transgene cassette (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon, or other nucleic acid element), based on a trait which permits the survival of the organism in an otherwise hostile or toxic environment (*e.g.*, in the presence of an antimicrobial compound). By employing one or more of the genes of the invention as genetic markers, the speed and ease with which organisms having desirable transformed traits (*e.g.*, modulated fine chemical production) are engineered and isolated are improved. While it is advantageous to use the genes of the invention for selection of transformed *C. glutamicum* and related bacteria, it is possible, as described herein, to use homologs (*e.g.*, homologs from other organisms), allelic variants or fragments of the gene retaining desired activity. Furthermore, 5' and 3' regulatory elements of the genes of the invention may be modified as described herein (*e.g.*, by nucleotide substitution, insertion, deletion, or replacement with a more desirable genetic element) to modulate the transcription of the gene. For example, an LMRB variant in which the nucleotide sequence in the region from -1 to -200 5' to the start codon has been altered to modulate (preferably increase) the transcription and/or translation of LMRB may be employed, as can constructs in which a gene of the invention (*e.g.*, the LMRB gene (SEQ ID NO:1)) is functionally coupled to one or more regulatory signals (*e.g.*, inducer or repressor binding sequences) which can be used for modulating gene expression.

Similarly, more than one copy of a gene (functional or inactivated) of the invention may be employed.

An additional application of the genes of the invention (*e.g.*, the gene encoding LMRB (SEQ ID NO:1) or other drug- or antibiotic-resistance gene) is in the discovery of new antibiotics which are active against *Corynebacteria* and/or other bacteria. For example, a gene of the invention may be expressed (or overexpressed) in a suitable host to generate an organism with increased resistance to one or more drugs or antibiotics (in the case of LMRB, lincosamides in particular, especially lincomycin). This type of resistant host can subsequently be used to screen for chemicals with bacteriostatic and/or bacteriocidal activity, such as novel antibiotic compounds. It is possible, in particular, to use the genes of the invention (*e.g.*, the LMRB gene) to identify new antibiotics which are active against those microorganisms which are already resistant to standard antibiotic compounds.

The invention provides methods for screening molecules which modulate the activity of an SRT protein, either by interacting with the protein itself or a substrate or binding partner of the SRT protein, or by modulating the transcription or translation of a SRT nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more SRT proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the SRT protein is assessed.

Manipulation of the SRT nucleic acid molecules of the invention may result in the production of SRT proteins having functional differences from the wild-type SRT proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity. The goal of such manipulations is to increase the viability and activity of the cell when the cell is exposed to the environmental and chemical stresses and hazards which frequently accompany large-scale fermentative culture. Thus, by increasing the activity or copy number of a heat-shock-regulated protease, one may increase the ability of the cell to destroy incorrectly folded proteins, which may otherwise interfere with normal cellular functioning (for example, by continuing to bind substrates or cofactors although the protein lacks the activity to act on these molecules appropriately). The same is true for the overexpression or optimization of activity of one or more chaperone molecules induced by heat or cold shock. These proteins aid in the correct folding of nascent polypeptide chains, and thus their increased activity or presence should increase the percentage of correctly folded proteins in the cell, which in turn should increase the overall metabolic efficiency and viability of the cells in culture. The overexpression or optimization of the transporter molecules activated by osmotic shock should result in an increased ability on the part of the cell to maintain intracellular homeostasis, thereby increasing the viability of these cells in culture. Similarly, the overproduction or

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increase in activity by mutagenesis of proteins involved in the development of cellular resistance to chemical stresses of various kinds (either by transport of the offending chemical out of the cell or by modification of the chemical to a less hazardous substance) should increase the fitness of the organism in the environment containing the hazardous substance (*i.e.*, large-scale fermentative culture), and thereby may permit relatively larger numbers of cells to survive in such a culture. The net effect of all of these mutagenesis strategies is to increase the quantity of fine-chemical-producing compounds in the culture, thereby increasing the yield, production, and/or efficiency of production of one or more desired fine chemicals from the culture.

This aforementioned list of mutagenesis strategies for SRT proteins to result in increased yields of a desired compound is not meant to be limiting; variations on these mutagenesis strategies will be readily apparent to one of ordinary skill in the art. By these mechanisms, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated SRT nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, Appendices, and the sequence listing cited throughout this application are hereby incorporated by reference.

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l MgSO₄ x 7H₂O, 10 ml/l KH₂PO₄ solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l (NH₄)₂SO₄, 1 g/l NaCl, 2 g/l MgSO₄ x 7H₂O, 0.2 g/l CaCl₂, 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l FeSO₄,

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x H₂O, 10 mg/l ZnSO₄ x 7 H₂O, 3 mg/l MnCl₂ x 4 H₂O, 30 mg/l H₃BO₃, 20 mg/l CoCl₂ x 6 H₂O, 1 mg/l NiCl₂ x 6 H₂O, 3 mg/l Na₂MoO₄ x 2 H₂O, 500 mg/l complexing agent (EDTA or citric acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30 min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCosI (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries

specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

- 5 Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see *e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-
- 10 GGAAACAGTATGACCATG-3' or 5'-GTAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

- In vivo* mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g.* *Bacillus* spp. or
- 15 yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such
- 20 strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

- Several *Corynebacterium* and *Brevibacterium* species contain endogenous
- 25 plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in
- 30 Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903
- 35 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E.*

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coli and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

- 5 Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vector into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases
10 where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an *Mcr*-deficient
15 *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

- Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be
20 overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

- Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known
25 methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as
30 homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH:
35 Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex

compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach" (eds. P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH_4OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex

compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2.5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's

Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays).

- 5 The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

- 10 The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

15 **Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product**

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

- 20 Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream
25 processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes
30 Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the

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production of the desired compound, such as intermediates and side-products, to determine the overall yield, production, and/or efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (e.g., sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum* cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. Biochemical Engineering Fundamentals, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994)

Appl. Environ. Microbiol. 60: 133-140; Malakhova *et al.* (1996) *Biotechnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

EXAMPLE 11: Cloning of a *Corynebacterium glutamicum* Gene Involved in Lincomycin Resistance Using a Reporter Gene Approach

A. Identification of the Gene Encoding the LMRB Protein

Plasmid pSL130 was constructed by ligation of the aceB promoter region (paceB) of *C. glutamicum* (Kim, H.J. *et al.* (1997) *J. Microbiol. Biotechnol.* 7: 287-292) into the polylinker of the lac operon fusion vector pRS415, which lacks a promoter (Simon, R.W. *et al.* (1987) *Gene* 53: 85-96). Plasmid pSL145 was constructed by ligating the resulting paceB-lac region into the *E. coli* cloning vector pACYC184. *E. coli* DH5αF' was transformed with pSL145 and the resulting strain was used as a host for screening of a genomic *C. glutamicum* library (in pSL109).

Transformants were screened by growth on agar medium containing 5-bromo-4-chloro-3-indolyl-beta-D-galactopyranoside (X-Gal). A white colony, containing DNA influencing lacZ expression, was selected for further analysis. This clone was found to contain a 4 kB fragment from the gene library. Subclones were constructed in pSL109 and a subclone which retained the white phenotype on X-Gal plates was identified. This subclone was found to contain a 2.6 kB BamHI-XhoI fragment (plasmid pSL149-5). The fragment was sequenced and identified as a membrane protein-encoding gene (LMRB gene).

The 1442 nucleotides of the coding sequence of the LMRB gene encode a polypeptide of 481 amino acid residues with a high percentage of hydrophobic amino acids. A Genbank search determined that the LMRB protein is 40% identical to the protein product of the lmrB gene from *Bacillus subtilis* (Genbank Accession AL009126, TREMBL Accession P94422), as determined using a CLUSTAL W analysis (using standard parameters).

The LMRN protein contains a sequence pattern: 158-A-P-A-L-G-P-T-L-S-G-167 (SEQ ID NO:301), which resembles the known multi-drug-resistance-protein consensus motif G-X-X-X-G-P-X-X-G-G (SEQ ID NO:302) (Paulsen, I.T., and Skurray, R.A.

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(1993) *Gene* 124: 1-11). Therefore, the LMRB protein was classified as a drug resistance protein.

B. In vivo Analysis of *lmrB* Function

- 5 The *lmrB* gene was overexpressed in *C. glutamicum* ASO19E12 (Kim, H.J. *et al.* (1997) *J. Microbiol. Biotechnol.* 7: 287-292) using the plasmid pSL149-5, described above.

- Disruption of the LMRB gene was accomplished by use of the vector pSL18-
lmrB. This vector was constructed as follows: an internal fragment of the LMRB gene
10 was amplified by PCR under standard conditions using primers 5'-
CTCCAGGATTGCTCCGAAGG-3' (SEQ ID NO:303) and 5'-
CACAGTGGTTGACCACTGGC-3' (SEQ ID NO:304). The resulting PCR product
was treated with T7 DNA polymerase and T7 polynucleotide kinase, and was cloned
into the *Sma*I site of plasmid pSL18 (Kim, Y.H. and H.-S. Lee (1996) *J. Microbiol.*
15 *Biotechnol.* 6: 315-320). The disruption of the LMRB gene in *C. glutamicum*
ASO19E12 was performed by conjugation, as previously described (Schwarzer and
Puhler (1991) *Bio/Technology* 9:84-87).

- C. glutamicum* cells transformed with pSL149-5 displayed similar resistances as
untransformed cells against erythromycin, penicillin G, tetracycline, chloramphenicol,
20 spectinomycin, nalidixic acid, gentamycin, streptomycin, ethidium bromide, carbonyl
cyanide m-chlorophenylhydrazone (CCCP), and sodium dodecyl sulfate. Significant
differences were observed, however, in the resistance of transformed and untransformed
cells to lincomycin.

- LMRB-overexpressing *C. glutamicum* cells were found to be able to grow in the
25 presence of 20 µg/ml lincomycin. In contrast, cells which do not overexpress LMRB (or
cells carrying a LMRB disruption) were not able to grow on agar media containing 5
µg/ml lincomycin. This effect was clearly visible in liquid culture. LMRB
overexpression led to a 9-fold increased resistance (compared to wild-type) against
lincomycin and LMRB disruption resulted in a decreased resistance (28% of wild-type)
30 to this antibiotic.

Example 12: Analysis of the Gene Sequences of the Invention

- The comparison of sequences and determination of percent homology between
two sequences are art-known techniques, and can be accomplished using a mathematical
35 algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci.*
USA 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* USA
90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST

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programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to SRT nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to SRT protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM, described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was

subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 13: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, e.g., Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium

described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 14: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those

proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18:

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1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

- The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (e.g., different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (e.g., metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

- Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

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What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a stress, resistance, or tolerance gene, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said stress, resistance, or tolerance gene is selected from the group consisting of nucleic acid molecules involved in a stress response, tolerance, or resistance to temperature stresses, pH stresses, oxygen stresses, osmotic stresses, toxic chemicals, oxygen radicals, antibiotics, or to lincomycin.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group

consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of
5 any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1
or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
- 10 10. A vector comprising the nucleic acid molecule of claim 1.
11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
- 15 13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium*
or *Brevibacterium*.
- 20 15. The host cell of claim 12, wherein the expression of said nucleic acid molecule
results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group
25 consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine
and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated
fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors,
polyketides, and enzymes.
- 30 17. A method of producing a polypeptide comprising culturing the host cell of claim 12
in an appropriate culture medium to, thereby, produce the polypeptide.
18. An isolated stress, resistance, or tolerance polypeptide from *Corynebacterium*
glutamicum, or a portion thereof.
- 35 19. The protein of claim 18, wherein said stress, resistance, or tolerance polypeptide is
selected from the group consisting of proteins involved in a stress response,

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tolerance, or resistance to temperature stresses, pH stresses, oxygen stresses, osmotic stresses, toxic chemicals, oxygen radicals, antibiotics, or to lincomycin.

- 5 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 10 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 15 22. The isolated polypeptide of claim 18, further comprising heterologous amino acid sequences.
- 20 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.
- 25 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 30 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 35 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.

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Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group
5 consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule is disrupted.

37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth in Appendix A.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

**CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
RESISTANCE AND TOLERANCE PROTEINS**

Abstract of the Disclosure

5

Isolated nucleic acid molecules, designated SRT nucleic acid molecules, which encode novel SRT proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SRT nucleic acid molecules, and host cells into which the expression

10 vectors have been introduced. The invention still further provides isolated SRT proteins, mutated SRT proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SRT genes in this organism.

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DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS, RESISTANCE, AND TOLERANCE PROTEINS

X is attached hereto.

was filed on _____ as _____

Application Serial No. _____

and was amended on _____
(if applicable)

I do not know and do not believe that the subject matter of this application was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date of this application, or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date of this application on an application filed more than twelve months (six months if this application is for a design) before the filing of this application; and I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application, that no application for patent or inventor's certificate on the subject matter of this application has been filed by me or my representatives or assigns in any country foreign to the United States, except those identified below, and that I have reviewed and understand the contents of the specification, including the claims as amended by any amendment referred to herein.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

CLAIM OF BENEFIT OF EARLIER FOREIGN APPLICATION(S)

I hereby claim priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below, and have also identified below any foreign application(s) for patent or inventor's certificate filed by me on the same subject matter having a filing date before that of the application(s) from which priority is claimed.

Check one:

☐ no such applications have been filed.

☒ such applications have been filed as follows

**EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED WITHIN 12 MONTHS
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION**

Country	Application Number	Date of Filing (month,day,year)	Priority Claimed Under 35 USC 119
DE	19930429.7	07/01/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931413.6	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931457.8	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931541.8	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19932209.0	07/09/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19932230.9	07/09/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19932914.1	07/14/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19940764.9	08/27/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19941382.7	08/31/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>

**ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION**

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CLAIM FOR BENEFIT OF U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

60/141,031
(Application Serial No.)

June 25, 1999
(Filing Date)

60/142,692
(Application Serial No.)

July 1, 1999
(Filing Date)

60/151,214
(Application Serial No.)

August 27, 1999
(Filing Date)

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CLAIM FOR BENEFIT OF EARLIER U.S./PCT APPLICATION(S)

I hereby claim the benefit under Title 35, United States Code, §120 of any earlier United States application(s) or PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the earlier application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date(s) of the earlier application(s) and the national or PCT international filing date of this application. As to subject matter of this application which is common to my earlier application(s), if any, described below, I do not know and do not believe that the same was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date(s) of said earlier application(s), or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date(s) of said earlier application(s) on an application filed more than twelve months (six months if this application is for a design) before the filing of said earlier application(s); and I acknowledge that no application for patent or inventor's certificate on said subject matter has been filed by me or my representatives or assigns in any country foreign to the United States except those identified herein.

 (Application Serial No.)

 (Filing Date)

 (Status)
 (patented,pending,aband.)

 (Application Serial No.)

 (Filing Date)

 (Status)
 (patented,pending,aband.)

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POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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Citizenship South Korea	
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SEQUENCE LISTING

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 70 75 80 85

 act aag acg atc ttt gtt act gcg ttg ttg ttc ttt acg gtt ggt acg 403
 Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe Phe Thr Val Gly Thr
 90 95 100

 ttg act gcg gcg ttg gct cca acg ttt gcg gtg ctg ctt ggt gct cgt 451
 Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val Leu Leu Gly Ala Arg
 105 110 115

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atc gtt cag gcg gtt ggt act gcg ctg gtg atg cct ttg ctg atg acg 499
 Ile Val Gln Ala Val Gly Thr Ala Leu Val Met Pro Leu Leu Met Thr
 120 125 130

gtt acg ttg acg gtg gtt cct gcg gag cgt cgt ggt tcg atg atg ggc 547
 Val Thr Leu Thr Val Val Pro Ala Glu Arg Arg Gly Ser Met Met Gly
 135 140 145

att att tcc atc gtg att tct gtt gcg ccg gcg ctt ggt cct acg ttg 595
 Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala Leu Gly Pro Thr Leu
 150 155 160 165

tct ggt gtc att ctt aac tct ttg acc tgg cac tgg ttg ttt tgg atg 643
 Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His Trp Leu Phe Trp Met
 170 175 180

atg ctt ccg atc gtt gtt atc gct ttg gta att ggt ttc ttc ttg atc 691
 Met Leu Pro Ile Val Val Ile Ala Leu Val Ile Gly Phe Phe Leu Ile
 185 190 195

aaa aat atc ggc gaa acc aag atc acc cca ctg gat gtt ctg tct gtc 739
 Lys Asn Ile Gly Glu Thr Lys Ile Thr Pro Leu Asp Val Leu Ser Val
 200 205 210

atc ctt tcg gtg ttt gcc ttc ggt ggt ttg gtg tac ggc ttc agt tcc 787
 Ile Leu Ser Val Phe Ala Phe Gly Gly Leu Val Tyr Gly Phe Ser Ser
 215 220 225

ttc gga gca atc ctg gag ggc gaa ggc acc gta ggt atc ttc gcg atc 835
 Phe Gly Ala Ile Leu Glu Gly Glu Gly Thr Val Gly Ile Phe Ala Ile
 230 235 240 245

gtc gtt ggc gcc atc gca ctc ctc atc ttt gct ttg cga cag cac caa 883
 Val Val Gly Ala Ile Ala Leu Leu Ile Phe Ala Leu Arg Gln His Gln
 250 255 260

ctc ggc aag caa gac aaa gca ctg atg gat ctc cga gcc ttc aag gtg 931
 Leu Gly Lys Gln Asp Lys Ala Leu Met Asp Leu Arg Ala Phe Lys Val
 265 270 275

agg aac ttc agc ttc tcc ttg acc acc atc ctt ttg gcg ttc ggc gcg 979
 Arg Asn Phe Ser Phe Ser Leu Thr Thr Ile Leu Leu Ala Phe Gly Ala
 280 285 290

atg ctc gga acc gtc atg gtt ttg cca atc tac ctg cag act tcc ctc 1027
 Met Leu Gly Thr Val Met Val Leu Pro Ile Tyr Leu Gln Thr Ser Leu
 295 300 305

gga gtt act gct ttg gtg acc ggt ttg gtt gtt atg ccc ggc ggc ctc 1075
 Gly Val Thr Ala Leu Val Thr Gly Leu Val Val Met Pro Gly Gly Leu
 310 315 320 325

ctc cag ggt ctg atc agc cca ttc atc gga cgt ttc tac gac aag gtc 1123
 Leu Gln Gly Leu Ile Ser Pro Phe Ile Gly Arg Phe Tyr Asp Lys Val
 330 335 340

ggt cca cgt ccg ctg ctg att ccc gga gca att gcg ctg gct atc gcg 1171
 Gly Pro Arg Pro Leu Leu Ile Pro Gly Ala Ile Ala Leu Ala Ile Ala
 345 350 355

gca tcc tcg atg act ttt ctc aat gag aat tca ccc gtg tgg atg gtc 1219

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Ala Ser Ser Met Thr Phe Leu Asn Glu Asn Ser Pro Val Trp Met Val
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gtg gtc atg cac gtt gtg ttc agc atc ggc atg tgt ttg atg atg acc 1267
 Val Val Met His Val Val Phe Ser Ile Gly Met Cys Leu Met Met Thr
 375 380 385

cct ctc atg acc acc gct ctc ggc gcc ctt ccg aag cac ctc tat ggt 1315
 Pro Leu Met Thr Thr Ala Leu Gly Ala Leu Pro Lys His Leu Tyr Gly
 390 395 400 405

cac ggc tcc gca att ttg aac acg ttc caa cag ctc gca ggc gca gcc 1363
 His Gly Ser Ala Ile Leu Asn Thr Phe Gln Gln Leu Ala Gly Ala Ala
 410 415 420

gga aca gcg atc atg att gca gca ctt tcc ttc ggc act tcc att gca 1411
 Gly Thr Ala Ile Met Ile Ala Ala Leu Ser Phe Gly Thr Ser Ile Ala
 425 430 435

gcg tct tcg gga tct gcg cat gct gaa gct gtt gcc gct ggt acc aag 1459
 Ala Ser Ser Gly Ser Ala His Ala Glu Ala Val Ala Ala Gly Thr Lys
 440 445 450

gtt gcg ttc atc gca ggc gca atc atc gcg gtg atc gct ttg gtt gtt 1507
 Val Ala Phe Ile Ala Gly Ala Ile Ile Ala Val Ile Ala Leu Val Val
 455 460 465

tcc ctc ttc gtc act cgc gtc gag gaa gaa gct cac taaataccaa 1553
 Ser Leu Phe Val Thr Arg Val Glu Glu Glu Ala His
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aaaatggggc aga 1566

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2
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Pro Arg Glu Val Val Val Val Leu Ser Ile Leu Val Val Ser Ala Met
 20 25 30

Ile Met Ile Leu Asn Glu Thr Ile Leu Ser Val Ala Leu Pro Ser Ile
 35 40 45

Met Glu Asp Phe Ser Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr
 50 55 60

Gly Phe Met Leu Thr Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu
 65 70 75 80

Leu Asp Arg Phe Ser Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe
 85 90 95

Phe Thr Val Gly Thr Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val
 100 105 110

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Leu Leu Gly Ala Arg Ile Val Gln Ala Val Gly Thr Ala Leu Val Met
 115 120
 Pro Leu Leu Met Thr Val Thr Leu Thr Val Val Pro Ala Glu Arg Arg
 130 135 140
 Gly Ser Met Met Gly Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala
 145 150 155 160
 Leu Gly Pro Thr Leu Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His
 165 170 175
 Trp Leu Phe Trp Met Met Leu Pro Ile Val Val Ile Ala Leu Val Ile
 180 185 190
 Gly Phe Phe Leu Ile Lys Asn Ile Gly Glu Thr Lys Ile Thr Pro Leu
 195 200 205
 Asp Val Leu Ser Val Ile Leu Ser Val Phe Ala Phe Gly Gly Leu Val
 210 215 220
 Tyr Gly Phe Ser Ser Phe Gly Ala Ile Leu Glu Gly Glu Gly Thr Val
 225 230 235 240
 Gly Ile Phe Ala Ile Val Val Gly Ala Ile Ala Leu Leu Ile Phe Ala
 245 250 255
 Leu Arg Gln His Gln Leu Gly Lys Gln Asp Lys Ala Leu Met Asp Leu
 260 265 270
 Arg Ala Phe Lys Val Arg Asn Phe Ser Phe Ser Leu Thr Thr Ile Leu
 275 280 285
 Leu Ala Phe Gly Ala Met Leu Gly Thr Val Met Val Leu Pro Ile Tyr
 290 295 300
 Leu Gln Thr Ser Leu Gly Val Thr Ala Leu Val Thr Gly Leu Val Val
 305 310 315 320
 Met Pro Gly Gly Leu Leu Gln Gly Leu Ile Ser Pro Phe Ile Gly Arg
 325 330 335
 Phe Tyr Asp Lys Val Gly Pro Arg Pro Leu Leu Ile Pro Gly Ala Ile
 340 345 350
 Ala Leu Ala Ile Ala Ala Ser Ser Met Thr Phe Leu Asn Glu Asn Ser
 355 360 365
 Pro Val Trp Met Val Val Val Met His Val Val Phe Ser Ile Gly Met
 370 375 380
 Cys Leu Met Met Thr Pro Leu Met Thr Thr Ala Leu Gly Ala Leu Pro
 385 390 395 400
 Lys His Leu Tyr Gly His Gly Ser Ala Ile Leu Asn Thr Phe Gln Gln
 405 410 415
 Leu Ala Gly Ala Ala Gly Thr Ala Ile Met Ile Ala Ala Leu Ser Phe
 420 425 430
 Gly Thr Ser Ile Ala Ala Ser Ser Gly Ser Ala His Ala Glu Ala Val

00603208.062300

435 440 445

Ala Ala Gly Thr Lys Val Ala Phe Ile Ala Gly Ala Ile Ile Ala Val
450 455 460

Ile Ala Leu Val Val Ser Leu Phe Val Thr Arg Val Glu Glu Glu Ala
465 470 475 480

His

<210> 3
<211> 371
<212> DNA
<213> *Corynebacterium glutamicum*

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<222> (52)..(348)
<223> RXA00497

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Asn Val Asn Ile Lys Pro Leu Glu Asp Lys Ile Leu Val Gln Ile Asn
5 10 15

gaa gca gag acc acc acc gct tcc ggc ctg gtc att cca gat tcc gct 153
Glu Ala Glu Thr Thr Thr Ala Ser Gly Leu Val Ile Pro Asp Ser Ala
20 25 30

aag gaa aag cca caa gag gca acc gtt atc gca gtt ggc cca ggc cgc 201
Lys Glu Lys Pro Gln Glu Ala Thr Val Ile Ala Val Gly Pro Gly Arg
35 40 45 50

ttc gat gac aag ggt aac cgc atc cca ctg gac atc aag gaa gat gac 249
Phe Asp Asp Lys Gly Asn Arg Ile Pro Leu Asp Ile Lys Glu Asp Asp
55 60 65

gtt gtg atc ttc tcc cgt tac ggc ggc acc gag atc aag ttc ggt ggc 297
Val Val Ile Phe Ser Arg Tyr Gly Gly Thr Glu Ile Lys Phe Gly Gly
70 75 80

gtg gag tac ttg ctt ctc tcc gct cgt gac atc ctc gca atc gtc gag 345
Val Glu Tyr Leu Leu Leu Ser Ala Arg Asp Ile Leu Ala Ile Val Glu
85 90 95

aag taggggataa gttcatggca aag 371
Lys

<210> 4
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<212> PRT
<213> *Corynebacterium glutamicum*

09603208.062300

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 20 25 30

Ser Ala Lys Glu Lys Pro Gln Glu Ala Thr Val Ile Ala Val Gly Pro
 35 40 45

Gly Arg Phe Asp Asp Lys Gly Asn Arg Ile Pro Leu Asp Ile Lys Glu
 50 55 60

Asp Asp Val Val Ile Phe Ser Arg Tyr Gly Gly Thr Glu Ile Lys Phe
 65 70 75 80

Gly Gly Val Glu Tyr Leu Leu Leu Ser Ala Arg Asp Ile Leu Ala Ile
 85 90 95

Val Glu Lys

<210> 5

<211> 1737

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1714)

<223> RXN00493

<400> 5

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gtgacatcct cgcaatcgct gagaagtagg ggataagttc atg gca aag ctc att 115
 Met Ala Lys Leu Ile
 1 5

gct ttt gac cag gac gcc cgc gaa ggc att ctc cgg ggc gtt gac gct 163
 Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu Arg Gly Val Asp Ala
 10 15 20

ctg gca aac gct gtc aag gta acc ctc ggc cca cgc ggc cgt aac gtg 211
 Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Arg Gly Arg Asn Val
 25 30 35

gtt ctt gat aag gca ttc ggc gga cct ctg gtc acc aac gac ggt gtc 259
 Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val Thr Asn Asp Gly Val
 40 45 50

acc att gcc cgc gac atc gac ctt gag gat cct ttt gag aac ctc ggt 307
 Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly
 55 60 65

gcg cag ctg gtg aag tcc gtt gct gtt aag acc aac gac atc gct ggt 355
 Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr Asn Asp Ile Ala Gly
 70 75 80 85

gac ggc acc acg act gca act ctg ctt gct cag gca ctc att gct gaa 403

002250.80230960

Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln Ala Leu Ile Ala Glu
 90 95 100
 ggc ctg cgc aac gtt gct gct ggc gca aac cca atg gag ctc aac aag 451
 Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro Met Glu Leu Asn Lys
 105 110 115
 ggt att tct gca gct gca gaa aag acc ttg gaa gag ttg aag gca cgc 499
 Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu Glu Leu Lys Ala Arg
 120 125 130
 gca acc gag gtg tct gac acc aag gaa atc gca aac gtc gct acc gtt 547
 Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala Asn Val Ala Thr Val
 135 140 145
 tca tcc cgc gat gaa gtt gtc ggc gag atc gtt gct gca cgc atg gaa 595
 Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val Ala Ala Ala Met Glu
 150 155 160 165
 aag gtt ggc aag gac ggt gtc gtc acc gtt gag gag tcc cag tcc atc 643
 Lys Val Gly Lys Asp Gly Val Val Thr Val Glu Glu Ser Gln Ser Ile
 170 175 180
 gag act gct ctc gag gtc acc gaa ggt att tct ttc gac aag ggc tac 691
 Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser Phe Asp Lys Gly Tyr
 185 190 195
 ctt tcc cct tat ttc atc aac gac aac gac act cag cag gct gtc ctg 739
 Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr Gln Ala Val Leu
 200 205 210
 gac aac cct gca gtg ctg ctt gtt cgc aac aag att tct tcc ctc cca 787
 Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys Ile Ser Ser Leu Pro
 215 220 225
 gac ttc ctc cca ttg ctg gag aag gtt gtg gag tcc aac cgt cct ttg 835
 Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu Ser Asn Arg Pro Leu
 230 235 240 245
 ctg atc atc gca gaa gac gtc gag ggc gag cct ttg cag acc ctg gtt 883
 Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro Leu Gln Thr Leu Val
 250 255 260
 gtg aac tcc atc cgc aag acc atc aag gtc gtt gca gtg aag tcc cct 931
 Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val Ala Val Lys Ser Pro
 265 270 275
 tac ttc ggt gac cga cgc aag cgc ttc atg gat gac ctg gct att gtc 979
 Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp Asp Leu Ala Ile Val
 280 285 290
 acc aag gca act gtc gtg gat cca gaa gtg ggc atc aac ctc aac gaa 1027
 Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly Ile Asn Leu Asn Glu
 295 300 305
 gct ggc gaa gaa gtt ttc ggt acc gca cgc cgc atc acc gtt tcc aag 1075
 Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg Ile Thr Val Ser Lys
 310 315 320 325
 gac gaa acc atc atc gtt gat ggt gca ggt tcc gca gaa gac gtt gaa 1123
 Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser Ala Glu Asp Val Glu

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330 335 340
 gca cgt cgc ggc cag atc cgt cgc gaa atc gcc aac acc gat tcc acc 1171
 Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala Asn Thr Asp Ser Thr
 345 350 355
 tgg gat cgc gaa aag gca gaa gag cgt ttg gct aag ctg tcc ggt ggt 1219
 Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala Lys Leu Ser Gly Gly
 360 365 370
 att gct gtc atc cgc gtt ggt gca gca act gaa acc gaa gtc aac gac 1267
 Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu Thr Glu Val Asn Asp
 375 380 385
 cgc aag ctg cgt gtc gaa gat gcc atc aac gct gct cgc gca gca gca 1315
 Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala Ala Arg Ala Ala Ala
 390 395 400 405
 caa gaa ggc gtt atc gct ggt ggc ggt tcc gct ttg gtt cag atc gct 1363
 Gln Glu Gly Val Ile Ala Gly Gly Gly Ser Ala Leu Val Gln Ile Ala
 410 415 420
 gag act ctg aag gct tac gcc gaa gag ttc gaa ggc gac cag aag gtc 1411
 Glu Thr Leu Lys Ala Tyr Ala Glu Glu Phe Glu Gly Asp Gln Lys Val
 425 430 435
 ggc gtt cgc gca ctg gct act gct ttg ggc aag cca gcg tac tgg atc 1459
 Gly Val Arg Ala Leu Ala Thr Ala Leu Gly Lys Pro Ala Tyr Trp Ile
 440 445 450
 gcc tcc aac gca ggt ctt gac ggc tct gtt gtt gtt gca cgc act gct 1507
 Ala Ser Asn Ala Gly Leu Asp Gly Ser Val Val Val Ala Arg Thr Ala
 455 460 465
 gct ctg cca aac ggc gag ggc ttc aac gct gca act ttg gaa tac gga 1555
 Ala Leu Pro Asn Gly Glu Gly Phe Asn Ala Ala Thr Leu Glu Tyr Gly
 470 475 480 485
 aac ctg atc aac gac ggt gtc atc gac cca gtc aag gtc acc cat tcc 1603
 Asn Leu Ile Asn Asp Gly Val Ile Asp Pro Val Lys Val Thr His Ser
 490 495 500
 gca gta gtg aat gca acc tct gtt gca cgc atg gtt ctg acc act gag 1651
 Ala Val Val Asn Ala Thr Ser Val Ala Arg Met Val Leu Thr Thr Glu
 505 510 515
 gct tct gtt gtt gag aag cct gca gaa gaa gca gcc gat gca cat gca 1699
 Ala Ser Val Val Glu Lys Pro Ala Glu Glu Ala Ala Asp Ala His Ala
 520 525 530
 gga cat cat cac cac taaagtctg tgaaaaaac cgt 1737
 Gly His His His
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<210> 6

<211> 538

<212> PRT

<213> Corynebacterium glutamicum

<400> 6

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Met Ala Lys Leu Ile Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu
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 Arg Gly Val Asp Ala Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro
 20 25 30
 Arg Gly Arg Asn Val Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val
 35 40 45
 Thr Asn Asp Gly Val Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro
 50 55 60
 Phe Glu Asn Leu Gly Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr
 65 70 75 80
 Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln
 85 90 95
 Ala Leu Ile Ala Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
 100 105 110
 Met Glu Leu Asn Lys Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu
 115 120 125
 Glu Leu Lys Ala Arg Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala
 130 135 140
 Asn Val Ala Thr Val Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val
 145 150 155 160
 Ala Ala Ala Met Glu Lys Val Gly Lys Asp Gly Val Val Thr Val Glu
 165 170 175
 Glu Ser Gln Ser Ile Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser
 180 185 190
 Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr
 195 200 205
 Gln Gln Ala Val Leu Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys
 210 215 220
 Ile Ser Ser Leu Pro Asp Phe Leu Pro Leu Glu Lys Val Val Glu
 225 230 235 240
 Ser Asn Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro
 245 250 255
 Leu Gln Thr Leu Val Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val
 260 265 270
 Ala Val Lys Ser Pro Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp
 275 280 285
 Asp Leu Ala Ile Val Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly
 290 295 300
 Ile Asn Leu Asn Glu Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg
 305 310 315 320
 Ile Thr Val Ser Lys Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser

00603200-062300

325 330 335

Ala Glu Asp Val Glu Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala
340 345 350

Asn Thr Asp Ser Thr Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala
355 360 365

Lys Leu Ser Ser Gly Gly Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu
370 375 380

Thr Glu Val Asn Asp Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala
385 390 395 400

Ala Arg Ala Ala Ala Gln Glu Gly Val Ile Ala Gly Gly Gly Ser Ala
405 410 415

Leu Val Gln Ile Ala Glu Thr Leu Lys Ala Tyr Ala Glu Glu Phe Glu
420 425 430

Gly Asp Gln Lys Val Gly Val Arg Ala Leu Ala Thr Ala Leu Gly Lys
435 440 445

Pro Ala Tyr Trp Ile Ala Ser Asn Ala Gly Leu Asp Gly Ser Val Val
450 455 460

Val Ala Arg Thr Ala Ala Leu Pro Asn Gly Glu Gly Phe Asn Ala Ala
465 470 475 480

Thr Leu Glu Tyr Gly Asn Leu Ile Asn Asp Gly Val Ile Asp Pro Val
485 490 495

Lys Val Thr His Ser Ala Val Val Asn Ala Thr Ser Val Ala Arg Met
500 505 510

Val Leu Thr Thr Glu Ala Ser Val Val Glu Lys Pro Ala Glu Glu Ala
515 520 525

Ala Asp Ala His Ala Gly His His His His
530 535

<210> 7
<211> 1339
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(1339)
<223> FRXA00498

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gtgacatcct cgcaatcgtc gagaagtagg ggataagttc atg gca aag ctc att 115
Met Ala Lys Leu Ile 5
1

gct ttt gac cag gac gcc cgc gaa ggc att ctc cgg ggc gtt gac gct 163
Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu Arg Gly Val Asp Ala

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ctg gca aac gct gtc aag gta acc ctc ggc cca cgc ggc cgt aac gtg				211
Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Arg Gly Arg Asn Val	25	30	35	
ggt ctt gat aag gca ttc ggc gga cct ctg gtc acc aac gac ggt gtc				259
Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val Thr Asn Asp Gly Val	40	45	50	
acc att gcc cgc gac atc gac ctt gag gat cct ttt gag aac ctc ggt				307
Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly	55	60	65	
gcg cag ctg gtg aag tcc gtt gct gtt aag acc aac gac atc gct ggt				355
Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr Asn Asp Ile Ala Gly	70	75	80	85
gac ggc acc acg act gca act ctg ctt gct cag gca ctc att gct gaa				403
Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln Ala Leu Ile Ala Glu	90	95	100	
ggc ctg cgc aac gtt gct gct ggc gca aac cca atg gag ctc aac aag				451
Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro Met Glu Leu Asn Lys	105	110	115	
ggt att tct gca gct gca gaa aag acc ttg gaa gag ttg aag gca cgc				499
Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu Glu Leu Lys Ala Arg	120	125	130	
gca acc gag gtg tct gac acc aag gaa atc gca aac gtc gct acc gtt				547
Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala Asn Val Ala Thr Val	135	140	145	
tca tcc cgc gat gaa gtt gtc ggc gag atc gtt gct gca gcg atg gaa				595
Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val Ala Ala Ala Met Glu	150	155	160	165
aag gtt ggc aag gac ggt gtc gtc acc gtt gag gag tcc cag tcc atc				643
Lys Val Gly Lys Asp Gly Val Val Thr Val Glu Glu Ser Gln Ser Ile	170	175	180	
gag act gct ctc gag gtc acc gaa ggt att tct ttc gac aag ggc tac				691
Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser Phe Asp Lys Gly Tyr	185	190	195	
ctt tcc cct tat ttc atc aac gac aac gac act cag cag gct gtc ctg				739
Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr Gln Ala Val Leu	200	205	210	
gac aac cct gca gtg ctg ctt gtt cgc aac aag att tct tcc ctc cca				787
Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys Ile Ser Ser Leu Pro	215	220	225	
gac ttc ctc cca ttg ctg gag aag gtt gtg gag tcc aac cgt cct ttg				835
Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu Ser Asn Arg Pro Leu	230	235	240	245
ctg atc atc gca gaa gac gtc gag ggc gag cct ttg cag acc ctg gtt				883
Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro Leu Gln Thr Leu Val	250	255	260	

00000000-00000000

gtg aac tcc atc cgc aag acc atc aag gtc gtt gca gtg aag tcc cct 931
Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val Ala Val Lys Ser Pro
265 270 275

tac ttc ggt gac cga cgc aag gcg ttc atg gat gac ctg gct att gtc 979
Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp Asp Leu Ala Ile Val
280 285 290

acc aag gca act gtc gtg gat cca gaa gtg ggc atc aac ctc aac gaa 1027
Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly Ile Asn Leu Asn Glu
295 300 305

gct ggc gaa gaa gtt ttc ggt acc gca cgc cgc atc acc gtt tcc aag 1075
Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg Ile Thr Val Ser Lys
310 315 320 325

gac gaa acc atc atc gtt gat ggt gca ggt tcc gca gaa gac gtt gaa 1123
Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser Ala Glu Asp Val Glu
330 335 340

gca cgt cgc ggc cag atc cgt cgc gaa atc gcc aac acc gat tcc acc 1171
Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala Asn Thr Asp Ser Thr
345 350 355

tgg gat cgc gaa aag gca gaa gag cgt ttg gct aag ctc tcc ggt ggt 1219
Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala Lys Leu Ser Gly Gly
360 365 370

att gct gtc atc cgc gtt ggt gca gca act gaa acc gaa gtc aac gac 1267
Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu Thr Glu Val Asn Asp
375 380 385

cgc aag ctg cgt gtc gaa gat gcc atc aac gct gct cgc gca gca gca 1315
Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala Ala Arg Ala Ala Ala
390 395 400 405

caa gaa ggc gtt atc gct ggt ggc 1339
Gln Glu Gly Val Ile Ala Gly Gly
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Arg Gly Val Asp Ala Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro
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Arg Gly Arg Asn Val Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val
35 40 45

Thr Asn Asp Gly Val Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro
50 55 60

Phe Glu Asn Leu Gly Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr

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Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr	Ala Thr Leu Leu Ala Gln																			
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Ala Leu Ile Ala Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro	110																			
Met Glu Leu Asn Lys Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu	115										120					125				
Glu Leu Lys Ala Arg Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala	130										135					140				
Asn Val Ala Thr Val Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val	145										150					155				
Ala Ala Ala Met Glu Lys Val Gly Lys Asp Gly Val Val Thr Val Glu	160										165					170				
Glu Ser Gln Ser Ile Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser	180										185					190				
Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr	195										200					205				
Gln Gln Ala Val Leu Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys	210										215					220				
Ile Ser Ser Leu Pro Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu	225										230					235				
Ser Asn Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro	245										250					255				
Leu Gln Thr Leu Val Val Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val	260										265					270				
Ala Val Lys Ser Pro Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp	275										280					285				
Asp Leu Ala Ile Val Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly	290										295					300				
Ile Asn Leu Asn Glu Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg	305										310					315				
Ile Thr Val Ser Lys Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser	325										330					335				
Ala Glu Asp Val Glu Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala	340										345					350				
Asn Thr Asp Ser Thr Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala	355										360					365				
Lys Leu Ser Gly Gly Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu	370										375					380				
Thr Glu Val Asn Asp Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala	385										390					395				
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 Met Ala Lys Tyr Gln
 1 5
 acc att gag gct gct gtc cgc tct gag ttc ggc aag ggc tct gca cgt 163
 Thr Ile Glu Ala Ala Val Arg Ser Glu Phe Gly Lys Gly Ser Ala Arg
 10 15 20
 cgt gca cgc gtt gct ggc cag atc cct gct gtt gtt tac ggc gca gat 211
 Arg Ala Arg Val Ala Gly Gln Ile Pro Ala Val Val Tyr Gly Ala Asp
 25 30 35
 gtt gag tcc aac ctg cac gtc acc atc gac cac cgc acc ttc gct gcg 259
 Val Glu Ser Asn Leu His Val Thr Ile Asp His Arg Thr Phe Ala Ala
 40 45 50
 ctg gtt cgc cag gaa ggc gta aac gct gtt ctt gag ctc gac atc gag 307
 Leu Val Arg Gln Glu Gly Val Asn Ala Val Leu Glu Leu Asp Ile Glu
 55 60 65
 ggc cag aag cag ctc acc atg atc aag cac atc gac cag aac gtg ctg 355
 Gly Gln Lys Gln Leu Thr Met Ile Lys His Ile Asp Gln Asn Val Leu
 70 75 80 85
 acc ttc cac atc gac cac ttg gac ctg ctt gcc att aag cgc ggc gaa 403
 Thr Phe His Ile Asp His Leu Asp Leu Leu Ala Ile Lys Arg Gly Glu
 90 95 100
 aag gtt gag gtt gac gtt cca gtt atc gtc gag ggc gag cca gct cca 451
 Lys Val Glu Val Asp Val Pro Val Ile Val Glu Gly Glu Pro Ala Pro
 105 110 115
 ggc acc atg tgg gtt cag gat gct gac acc atc aag gtt gag gct gac 499
 Gly Thr Met Trp Val Gln Asp Ala Asp Thr Ile Lys Val Glu Ala Asp
 120 125 130
 gtt ctg tcc atc cct gaa gag ttc acc gtt tcc atc gaa ggc ctt gag 547
 Val Leu Ser Ile Pro Glu Glu Phe Thr Val Ser Ile Glu Gly Leu Glu
 135 140 145
 ctc ggc gca cag atc acc gca gct gac atc aag ctc gag ggc gac acc 595
 Leu Gly Ala Gln Ile Thr Ala Ala Asp Ile Lys Leu Glu Gly Asp Thr
 150 155 160 165

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acc ctg gtt gag gat cct gag acc ctc atc gtc aac atc gtt ctc cca 643
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gct gtc gag gaa gaa gac acc gaa gag gac gaa gca gct gaa gaa gca 691
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gct act gag taagctttt tagatagctt tat 723
 Ala Thr Glu
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<212> PRT

<213> Corynebacterium glutamicum

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Lys Gly Ser Ala Arg Arg Ala Arg Val Ala Gly Gln Ile Pro Ala Val
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Val Tyr Gly Ala Asp Val Glu Ser Asn Leu His Val Thr Ile Asp His
 35 40 45

Arg Thr Phe Ala Ala Leu Val Arg Gln Glu Gly Val Asn Ala Val Leu
 50 55 60

Glu Leu Asp Ile Glu Gly Gln Lys Gln Leu Thr Met Ile Lys His Ile
 65 70 75 80

Asp Gln Asn Val Leu Thr Phe His Ile Asp His Leu Asp Leu Leu Ala
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Ile Lys Arg Gly Glu Lys Val Glu Val Asp Val Pro Val Ile Val Glu
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Gly Glu Pro Ala Pro Gly Thr Met Trp Val Gln Asp Ala Asp Thr Ile
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Lys Val Glu Ala Asp Val Leu Ser Ile Pro Glu Glu Phe Thr Val Ser
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Ile Glu Gly Leu Glu Leu Gly Ala Gln Ile Thr Ala Ala Asp Ile Lys
 145 150 155 160

Leu Glu Gly Asp Thr Thr Leu Val Glu Asp Pro Glu Thr Leu Ile Val
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Asn Ile Val Leu Pro Ala Val Glu Glu Glu Asp Thr Glu Glu Asp Glu
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Ala Ala Glu Glu Ala Ala Thr Glu
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cag Gln	tgg Trp	atc Ile	aac Asn 220	gct Ala 220	gaa Glu	ggt Gly	aag Lys	cca Pro	gtt Val 225	tgg Trp	gtt Val	aag Lys	tac Tyr	cac His 230	ttc Phe	725
aag Lys	acc Thr	cgc Arg	cag Gln 235	ggc Gly	tgg Trp	gat Asp	tgc Cys	ttc Phe 240	acc Thr	gat Asp	gca Ala	gaa Glu	gca Ala	gca Ala	aag Lys	773
gtt Val	gca Ala	ggc Gly 250	gag Glu	aac Asn	gct Ala	gac Asp	tac Tyr 255	cag Gln	cgc Arg	gaa Glu	gac Asp	ctc Leu 260	tac Tyr	aac Asn	gct Ala	821
att Ile	gaa Glu 265	aac Asn	ggc Gly	gac Asp	ttc Phe	cca Pro 270	atc Ile	tgg Trp	gac Asp	gtc Val 275	aag Lys	gtt Val	cag Gln	atc Ile	atg Met	869
cct Pro 280	ttc Phe	gag Glu	gat Asp	gca Ala	gag Glu 285	aac Asn	tac Tyr	cgc Arg	tgg Trp	aac Pro 290	cca Pro	ttc Phe	gac Asp	ctg Leu	acc Thr 295	917
aag Lys	acc Thr	tgg Trp	tcc Ser	cag Gln 300	aag Lys	gat Asp	tac Tyr	cca Pro	ctg Leu 305	atc Ile	cca Pro	gtc Val	ggt Gly	tac Tyr	ttc Phe 310	965
atc Ile	ctg Leu	aac Asn	cgc Arg 315	aac Asn	cca Pro	cgc Arg	aac Asn	ttc Phe 320	ttc Phe	gct Ala	cag Gln	atc Ile	gag Glu 325	cag Gln	ctt Leu	1013
gca Ala	ctg Leu	gat Asp 330	cca Pro	ggc Gly	aac Asn	atc Ile	gtt Val 335	cct Pro	ggc Gly	gtc Val	ggc Gly	ctg Leu 340	tcc Ser	cca Pro	gac Asp	1061
cgc Arg 345	atg Met	ctc Leu	cag Gln	gca Ala	cgt Arg	atc Ile 350	ttc Phe	gca Ala	tac Tyr	gct Ala	gac Asp 355	cag Gln	cag Gln	cgt Arg	tac Tyr	1109
cgc Arg 360	atc Ile	ggc Gly	gct Ala	aac Asn	tac Tyr 365	cgc Arg	gac Asp	ctg Leu	cca Pro	gtg Val 370	aac Asn	cgt Arg	cca Pro	atc Ile	aac Asn 375	1157
gag Glu	gtc Val	aac Asn	acc Thr 380	atc Ser	agc Ser	cgc Glu	gaa Glu	ggt Gly	tcc Ser 385	atg Met	cag Gln	tac Tyr	atc Ile	ttc Phe 390	gac Asp	1205
gct Ala	gag Glu	ggc Gly	gag Glu 395	cct Pro	tcc Ser	tac Tyr	agc Ser	cct Pro 400	aac Asn	cgc Arg	tac Tyr	gac Asp	aag Lys 405	ggc Gly	gca Ala	1253
ggc Gly	tac Tyr	ctg Leu 410	gat Asp	aac Asn	ggt Gly	acg Thr	gat Tyr 415	tcc Ser	tcc Ser	tcc Ser	aac Asn	cac His 420	acc His	tcc Ser	tac Tyr	1301
ggc Gly	cag Gln	gct Ala	gat Asp	gac Asp	atc Ile 430	tac Tyr	gtc Val	aac Asn	cca Pro	gac Asp	cca Pro 435	cac His	ggc Gly	acc Thr	gac Asp	1349

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ctg gtt cgt gct gct tac gtc aag cac cag gat gat gac gac ttc atc	1397
Leu Val Arg Ala Ala Tyr Val Lys His Gln Asp Asp Asp Phe Ile	
440 445	
cag cca ggc atc cta tac cgc gag gtc ctg gat gag ggc gag aag gag	1445
Gln Pro Gly Ile Leu Tyr Arg Glu Val Leu Asp Glu Gly Glu Lys Glu	
460 465 470	
cga ttg gca gac aac atc tcc aac gca atg cag ggc atc tct gag gca	1493
Arg Leu Ala Asp Asn Ile Ser Asn Ala Met Gln Gly Ile Ser Glu Ala	
475 480 485	
acc gag cca cgc gtc tac gac tac tgg aac aac gtt gat gag aac ctc	1541
Thr Glu Pro Arg Val Tyr Asp Trp Asn Asn Val Asp Glu Asn Leu	
490 495 500	
ggc gct cgc gtc aag gag ctt tac ctc cag aag aag gct taagtctctc	1590
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Ser Glu Asn Ile Ser Ala Thr Ala Gly Pro Gln Gly Pro Asn Val Leu
 35          40          45
Asn Asp Ile His Leu Ile Glu Lys Leu Ala His Phe Asn Arg Glu Asn
 50          55          60
Val Pro Glu Arg Ile Pro His Ala Lys Gly His Gly Ala Phe Gly Glu
 65          70          75
Leu His Ile Thr Glu Asp Val Ser Glu Tyr Thr Lys Ala Asp Leu Phe
 85          90          95
Gln Pro Gly Lys Val Thr Pro Leu Ala Val Arg Phe Ser Thr Val Ala
100          105          110
Gly Glu Gln Gly Ser Pro Asp Thr Trp Arg Asp Val His Gly Phe Ala
115          120          125
Leu Arg Phe Tyr Thr Glu Glu Gly Asn Tyr Asp Ile Val Gly Asn Asn
130          135          140
Thr Pro Thr Phe Phe Leu Arg Asp Gly Met Lys Phe Pro Asp Phe Ile
145          150          155          160
His Ser Gln Lys Arg Leu Asn Lys Asn Gly Leu Arg Asp Ala Asp Met
165          170          175

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Gln Trp Asp Phe Trp Thr Arg Ala Pro Glu Ser Ala His Gln Val Thr
 180 185 190
 Tyr Leu Met Gly Asp Arg Gly Thr Pro Lys Thr Ser Arg His Gln Asp
 195 200 205
 Gly Phe Gly Ser His Thr Phe Gln Trp Ile Asn Ala Glu Gly Lys Pro
 210 215 220
 Val Trp Val Lys Tyr His Phe Lys Thr Arg Gln Gly Trp Asp Cys Phe
 225 230 235 240
 Thr Asp Ala Glu Ala Ala Lys Val Ala Gly Glu Asn Ala Asp Tyr Gln
 245 250 255
 Arg Glu Asp Leu Tyr Asn Ala Ile Glu Asn Gly Asp Phe Pro Ile Trp
 260 265 270
 Asp Val Lys Val Gln Ile Met Pro Phe Glu Asp Ala Glu Asn Tyr Arg
 275 280 285
 Trp Asn Pro Phe Asp Leu Thr Lys Thr Trp Ser Gln Lys Asp Tyr Pro
 290 295 300
 Leu Ile Pro Val Gly Tyr Phe Ile Leu Asn Arg Asn Pro Arg Asn Phe
 305 310 315 320
 Phe Ala Gln Ile Glu Gln Leu Ala Leu Asp Pro Gly Asn Ile Val Pro
 325 330 335
 Gly Val Gly Leu Ser Pro Asp Arg Met Leu Gln Ala Arg Ile Phe Ala
 340 345 350
 Tyr Ala Asp Gln Gln Arg Tyr Arg Ile Gly Ala Asn Tyr Arg Asp Leu
 355 360 365
 Pro Val Asn Arg Pro Ile Asn Glu Val Asn Thr Tyr Ser Arg Glu Gly
 370 375 380
 Ser Met Gln Tyr Ile Phe Asp Ala Glu Gly Glu Pro Ser Tyr Ser Pro
 385 390 395 400
 Asn Arg Tyr Asp Lys Gly Ala Gly Tyr Leu Asp Asn Gly Thr Asp Ser
 405 410 415
 Ser Ser Asn His Thr Ser Tyr Gly Gln Ala Asp Asp Ile Tyr Val Asn
 420 425 430
 Pro Asp Pro His Gly Thr Asp Leu Val Arg Ala Ala Tyr Val Lys His
 435 440 445
 Gln Asp Asp Asp Asp Phe Ile Gln Pro Gly Ile Leu Tyr Arg Glu Val
 450 455 460
 Leu Asp Glu Gly Glu Lys Glu Arg Leu Ala Asp Asn Ile Ser Asn Ala
 465 470 475 480
 Met Gln Gly Ile Ser Glu Ala Thr Glu Pro Arg Val Tyr Asp Tyr Trp
 485 490 495

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Asn Asn Val Asp Glu Asn Leu Gly Ala Arg Val Lys Glu Leu Tyr Leu
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Gln Lys Lys Ala
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<223> RXA00404
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		Val Ala Leu Lys Arg 1 5
	ccc gaa gag aaa aca gta aag atc gtg acc ata aaa cag act gac aac	163
	Pro Glu Glu Lys Thr Val Lys Ile Val Thr Ile Lys Gln Thr Asp Asn	10 15 20
	atc aat gac gat gat ttg gtg tac agc aac gct act gac ctt cca gta	211
	Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala Thr Asp Leu Pro Val	25 30 35
	ggc gtg aag aag tcc cct aaa atg tca ccg acc gcc cgc gtt ggt ctc	259
	Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr Ala Arg Val Gly Leu	40 45 50
	ctt gtc ttt ggg gtt atc gcg gcg gtg ggt tgg gga gca atc gct ttc	307
	Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp Gly Ala Ile Ala Phe	55 60 65
	tcc cgt ggc gaa aca atc aac tct gtg tgg ctg gtt ttg gcg gca gtt	355
	Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu Val Leu Ala Ala Val	70 75 80 85
	ggt tcc tat atc att gcg ttt tct ttc tat gcc cga ctg att gaa tac	403
	Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala Arg Leu Ile Glu Tyr	90 95 100
	aaa gtt gtt aag ccg aaa gat cag cga gca acc ccg gcg gaa tac gtt	451
	Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr Pro Ala Glu Tyr Val	105 110 115
	aat gac gcc aag gac tat gtc cca acg gat cgt cgt gtg ctt ttt ggc	499
	Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg Arg Val Leu Phe Gly	120 125 130
	cac cac ttt gca gct att gca ggt gcc ggt cca ttg gtt gga cct gtc	547
	His His Phe Ala Ala Ile Ala Gly Ala Gly Pro Leu Val Gly Pro Val	135 140 145
	atg gcc gcg cag atg ggc tac ctg cca gcc acc ttg tgg att atc ctc	595

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ggt gtg att ttc gcc ggt gca gtg cag gac tac cta gtg ctg tgg gtg					643
Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr Leu Val Leu Trp Val	170	175		180	
tct act cgt agg cgt gga cgc tca ctt ggc cag atg gtt cgt gat gaa					691
Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln Met Val Arg Asp Glu	185	190		195	
atg ggc acg gtc ggt gga gct gcc ggt atc ttg gcg acc atc tcc atc					739
Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu Ala Thr Ile Ser Ile	200	205		210	
atg atc atc att atc gcg gtg ctc gca ttg atc gtg gtt aat gca ctg					787
Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile Val Val Asn Ala Leu	215	220		225	
gct gat tca cca tgg ggc gtt ttc tcc atc acc atg acc atc cca att					835
Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr Met Thr Ile Pro Ile	230	235		240	245
gca ctg ttc atg ggt gtg tac ttg cgt tac ctg cgc cca ggt cgt gtt					883
Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu Arg Pro Gly Arg Val	250	255		260	
act gaa gtg tcc atc atc ggt gtg gca ctg ctc ctg ctg gct atc gtt					931
Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu Leu Ala Ile Val	265	270		275	
gct ggt ggt tgg gtt gca gac acc tca tgg ggc gtg gaa tgg ttc acc					979
Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly Val Glu Trp Phe Thr	280	285		290	
tgg tct aag acc act ttg gcg ttg gcc ttg atc ggt tac gga atc atg					1027
Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile Gly Tyr Gly Ile Met	295	300		305	
gct gcg att ttg ccg gtg tgg ctg ctg ctt gca cgc cgc gat tac ctg					1075
Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala Pro Arg Asp Tyr Leu	310	315		320	325
tct acc ttt atg aag atc ggc gtc atc ggt ctg ttg gca gtg ggt att					1123
Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu Leu Ala Val Gly Ile	330	335		340	
ttg ttc gca cgt cct gag gtg cag atg cct tcc gtg acc tcc ttc gca					1171
Leu Phe Ala Arg Pro Gly Val Gln Met Pro Ser Val Thr Ser Phe Ala	345	350		355	
ctt gag ggc aac ggt ccg gtg ttc tct gga agt ctg ttc cca ttc ctg					1219
Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser Leu Phe Pro Phe Leu	360	365		370	
ttc atc acg att gcc tgt ggt gca ctg tct ggt ttc cac gca ctg att					1267
Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly Phe His Ala Leu Ile	375	380		385	
tct tca gga acc aca cca aag ctt gtg gag aag gaa tcc cag atg cgc					1315
Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys Glu Ser Gln Met Arg					

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390											395											400											405	
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Met	Leu	Gly	Tyr	Gly	Gly	Met	Leu	Met	Glu	Ser	Phe	Val	Ala	Met	Met																			
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Ala	Leu	Ile	Thr	Ala	Val	Ile	Leu	Asp	Arg	His	Leu	Tyr	Phe	Ser	Met																			
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aac	gct	ccg	ctg	gca	ctg	act	ggt	gga	gat	cca	gca	acc	gca	gct	gag	1459																		
Asn	Ala	Pro	Leu	Ala	Leu	Thr	Gly	Gly	Asp	Pro	Ala	Thr	Ala	Ala	Glu																			
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tgg	gtt	aac	tcc	att	ggg	ctg	aca	ggt	gcg	gat	atc	acc	ccg	gaa	cag	1507																		
Trp	Val	Asn	Ser	Ile	Gly	Leu	Thr	Gly	Ala	Asp	Ile	Thr	Pro	Glu	Gln																			
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ctg	tcg	gaa	gct	gct	gaa	agt	gtc	gga	gaa	tcc	act	gtt	att	tcc	cgt	1555																		
Leu	Ser	Glu	Ala	Ala	Glu	Ser	Val	Gly	Glu	Ser	Thr	Val	Ile	Ser	Arg																			
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acc	ggt	ggc	gca	cca	acc	tgt	gcg	ttc	ggt	atg	tct	gaa	atc	ctc	tcc	1603																		
Thr	Gly	Gly	Ala	Pro	Thr	Leu	Ala	Phe	Gly	Met	Ser	Glu	Ile	Leu	Ser																			
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gga	ttc	atc	ggc	ggc	gct	gga	atg	aag	gcg	ttc	tgg	tac	cac	ttc	gcc	1651																		
Gly	Phe	Ile	Gly	Gly	Ala	Gly	Met	Lys	Ala	Phe	Trp	Tyr	His	Phe	Ala																			
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atc	atg	ttt	gag	gct	ctg	ttc	atc	ctc	act	act	gtg	gat	gca	ggt	act	1699																		
Ile	Met	Phe	Glu	Ala	Leu	Phe	Ile	Leu	Thr	Thr	Val	Asp	Ala	Gly	Thr																			
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cgt	gtg	gct	cgc	ttt	atg	atg	acc	gat	acc	tgt	ggc	aat	gtt	cca	ggt	1747																		
Arg	Val	Ala	Arg	Phe	Met	Met	Thr	Asp	Thr	Leu	Gly	Asn	Val	Pro	Gly																			
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acc	gtg	ttt	gtg	tgt	gct	cta	tgg	ggt	gct	att	ttg	ctc	atg	ggt	gtt	1843																		
Thr	Val	Phe	Val	Cys	Ala	Leu	Trp	Gly	Ala	Ile	Leu	Leu	Met	Gly	Val																			
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Thr	Asp	Pro	Leu	Gly	Gly	Ile	Asn	Val	Leu	Phe	Pro	Leu	Phe	Gly	Ile																			
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gct	aac	cag	ctg	ctc	gcc	gct	att	gca	ctt	gct	ctc	gtg	ctg	gtt	gtt	1939																		
Ala	Asn	Gln	Leu	Leu	Ala	Ala	Ile	Ala	Leu	Ala	Leu	Val	Leu	Val	Val																			
				600													605													610				
gtg	gtg	aag	aag	ggc	ctg	tac	aag	tgg	gcg	tgg	att	cca	gct	gtt	cct	1987																		
Val	Val	Lys	Lys	Gly	Leu	Tyr	Lys	Trp	Ala	Trp	Ile	Pro	Ala	Val	Pro																			
				615													620																	

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Phe	His	Ser	Asp	650	Pro	Ala	Ile	Gly	Tyr	Trp	Ala	Gln	Asn	Ala	Asn	Phe
cgc	gat	gca	aag	tct	caa	ggc	ctt	acc	gaa	ttt	ggt	gcc	gct	aaa	tct	2131
Arg	Asp	Ala	Lys	665	Ser	Gln	Gly	Leu	Thr	Glu	Phe	Gly	Ala	Ala	Lys	Ser
cct	gag	gca	atc	gat	gcg	gtt	atc	cga	aac	acc	atg	att	cag	ggc	atc	2179
Pro	Glu	Ala	Ile	Asp	Ala	Val	Ile	Arg	Asn	Thr	Met	Ile	Gln	Gly	Ile	
ttg	tcc	atc	ctg	ttc	gcg	gtg	ctc	gtc	ctc	ggt	gtt	gtc	ggc	gca	gcc	2227
Leu	Ser	Ile	Leu	Phe	Ala	Val	Leu	Val	Leu	Val	Val	Val	Gly	Ala	Ala	
att	gcg	gtg	tgc	atc	aag	tcc	atc	agg	gct	cgt	gca	gcc	gga	aca	cct	2275
Ile	Ala	Val	Cys	Ile	Lys	Ser	Ile	Arg	Ala	Ala	Ala	Ala	Gly	Thr	Pro	
ttg	gag	acc	act	gaa	gag	cct	gat	act	gaa	tct	gag	ttc	ttc	gcc	cca	2323
Leu	Glu	Thr	Thr	Glu	Glu	Pro	Asp	Thr	Glu	Ser	Glu	Phe	Phe	Ala	Pro	
act	gga	ttc	ctt	gca	tct	tcc	agg	gat	aag	gaa	gtc	cag	gcc	atg	tgg	2371
Thr	Gly	Phe	745	Ala	Ser	Ser	Arg	Asp	Lys	Glu	Val	Gln	Ala	Met	Trp	
gac	gag	cgc	tac	cca	ggc	ggt	gcg	ccc	gtg	tct	tct	gga	ggg	cac		2416
Asp	Glu	Arg	Tyr	Pro	Gly	Gly	Ala	Pro	Val	Ser	Ser	Gly	Gly	His		
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Lys	Gln	Thr	Asp	Asn	Ile	Asn	Asp	Asp	Asp	Leu	Val	Tyr	Ser	Asn	Ala	
			20					25					30			
Thr	Asp	Leu	Pro	Val	Gly	Val	Lys	Lys	Ser	Pro	Lys	Met	Ser	Pro	Thr	
			35				40					45				
Ala	Arg	Val	Gly	Leu	Leu	Val	Phe	Gly	Val	Ile	Ala	Ala	Val	Gly	Trp	
			50				55				60					
Gly	Ala	Ile	Ala	Phe	Ser	Arg	Gly	Glu	Thr	Ile	Asn	Ser	Val	Trp	Leu	
					70					75					80	
Val	Leu	Ala	Ala	Val	Gly	Ser	Tyr	Ile	Ile	Ala	Phe	Ser	Phe	Tyr	Ala	
				85					90					95		
Arg	Leu	Ile	Glu	Tyr	Lys	Val	Val	Lys	Pro	Lys	Asp	Gln	Arg	Ala	Thr	

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Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro
 435 440 445
 Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp
 450 455 460
 Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser
 465 470 475 480
 Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met
 485 490 495
 Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe
 500 505 510
 Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr
 515 520 525
 Val Asp Ala Gly Thr Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu
 530 535 540
 Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val
 545 550 555 560
 Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile
 565 570 575
 Leu Leu Met Gly Val Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe
 580 585 590
 Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala
 595 600 605
 Leu Val Leu Val Val Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp
 610 615 620
 Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala
 625 630 635 640
 Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala
 645 650 655
 Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe
 660 665 670
 Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr
 675 680 685
 Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val
 690 695 700
 Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg
 705 710 715 720
 Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser
 725 730 735
 Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu
 740 745 750

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Val Gln Ala Met Trp Asp Glu Arg Tyr Pro Gly Gly Ala Pro Val Ser
755 760 765

Ser Gly Gly His
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atatgctcgg tgcgga aacc tacgaaagga ttttttaccg atg gct gta tac gaa 115
Met Ala Val Tyr Glu
1 5

ctc cca gaa ctc gac tac gca tac gac gct ctc gag cca cac atc gtc 163
Leu Pro Glu Leu Asp Tyr Ala Tyr Asp Ala Leu Glu Pro His Ile Val
10 15 20

gct gaa atc atg gag ctt gac cag tcc aag gac cac gca acc tac gtt 211
Ala Glu Ile Met Glu Leu Asp Gln Ser Lys Asp His Ala Thr Tyr Val
25 30 35

gcg ggc gca aat gca gca ctc taggcactag agaaggcacg cga 255
Ala Gly Ala Asn Ala Ala Leu
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<213> Corynebacterium glutamicum
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Met Ala Val Tyr Glu Leu Pro Glu Leu Asp Tyr Ala Tyr Asp Ala Leu
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Glu Pro His Ile Val Ala Glu Ile Met Glu Leu Asp Gln Ser Lys Asp
20 25 30

His Ala Thr Tyr Val Ala Gly Ala Asn Ala Ala Leu
35 40

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<222> (101)..(226)
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<223> RXN03120

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ccaggagggc aacatctcct tcgacatcac cccagttctg atg ctc gat atg tgg 115
Met Leu Asp Met Trp
1 5

gag cac gct ttc tac ctg cag tac atg aac gtt aag gca gat tac gtc 163
Glu His Ala Phe Tyr Leu Gln Tyr Met Asn Val Lys Ala Asp Tyr Val
10 15 20

aag gct gtt tgg aac gtc ttc aac tgg gac gac gca aga gca cgc ttc 211
Lys Ala Val Trp Asn Val Phe Asn Trp Asp Asp Ala Arg Ala Arg Phe
25 30 35

gca gca gct tcc aag taagcatttt tagtccgtgc aat 249
Ala Ala Ala Ser Lys
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<210> 18

<211> 42

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 18

Met Leu Asp Met Trp Glu His Ala Phe Tyr Leu Gln Tyr Met Asn Val
1 5 10 15

Lys Ala Asp Tyr Val Lys Ala Val Trp Asn Val Phe Asn Trp Asp Asp
20 25 30

Ala Arg Ala Arg Phe Ala Ala Ala Ser Lys
35 40

<210> 19

<211> 660

<212> DNA

<213> *Corvnebacterium glutamicum*

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<221> CDS

<222> (101) . . (637)

<223> RXN00575

<400> 19

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ccggttgccg atctatttaa ataccaggac aattgcgtgc atg gtt gaa aga gac 115
Met Val Glu Arg Asp
1 5

ttc act atc cga cca atc cgc gag ggt gat ttc cct cag gtg agg gac 163
Phe Thr Ile Arg Pro Ile Arg Glu Gly Asp Phe Pro Gln Val Arg Asp
10 15 20

atc tac gaa ttg ggc ctg gag acg gga cat gcg act tat gag act tct 211
Ile Tyr Glu Leu Gly Leu Glu Thr Gly His Ala Thr Tyr Glu Thr Ser

096030R DE200

	25								30							35						
ggt ccc acg tgg gac cag ttc tcc caa tct aaa atc atg gat acc gtc																						259
Gly Pro Thr Trp Asp Gln Phe Ser Gln Ser Lys Ile Met Asp Thr Val																						
40																						
atg gtg gcg gta gaa aac aac gac ccg gac ttc atc ctc gga tgg gtg																						307
Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu Gly Trp Val																						
55																						
tct gct gct cca att tca agc cga cag gtt ttc cat gga gtg gtg gaa																						355
Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly Val Val Glu																						
70																						
gat tcc atc tat atc cac ccc cag gcc caa gcc cga gga atc ggc gcc																						403
Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly Ile Gly Gly																						
90																						
gct ttg ctc gac gcc ctt atc acc tac tgc gaa agc aac ggc atc tgg																						451
Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn Gly Ile Trp																						
105																						
tcg atc cac tcc tgg atc ttc ccg gaa aac ctc ggt tct gcg aaa ctg																						499
Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser Ala Lys Leu																						
120																						
cat gaa tcg aag ggc ttc gtg aag gtg gcc acc atg cac caa atg gca																						547
His Glu Ser Lys Gly Phe Val Lys Val Gly Thr Met His Gln Met Ala																						
135																						
agg atg ccc tac ggc gag atg gaa gga caa tgg cgc gat tgt gat ctg																						595
Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp Cys Asp Leu																						
150																						
tgg gag tgc ctc tta tcc gtt cca gag caa gct caa agt tcc																						637
Trp Glu Cys Leu Leu Ser Val Pro Glu Gln Ala Gln Ser Ser																						
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Met Val Glu Arg Asp Phe Thr Ile Arg Pro Ile Arg Glu Gly Asp Phe																						
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Pro Gln Val Arg Asp Ile Tyr Glu Leu Gly Leu Glu Thr Gly His Ala																						
20																						
Thr Tyr Glu Thr Ser Gly Pro Thr Trp Asp Gln Phe Ser Gln Ser Lys																						
35																						
Ile Met Asp Thr Val Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe																						
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              Val Arg Asp Ile Tyr
              1                      5

gaa ttg  ggc  ctg  gag  acg  gga  cat  gcg  act  tat  gag  act  tct  ggt  ccc    163
Glu Leu Gly Leu Glu Thr Gly His Ala Thr Tyr Glu Thr Ser Gly Pro
              10                      20

acg tgg  gac  cag  ttc  tcc  caa  tct  aaa  atc  atg  gat  acc  gtc  atg  gtg    211
Thr Trp Asp Gln Phe Ser Gln Ser Lys Ile Met Asp Thr Val Met Val
              25                      30                      35

gcg gta  gaa  aac  aac  gac  ccg  gac  ttc  atc  ctc  gga  tgg  gtg  tct  gct    259
Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu Gly Trp Val Ser Ala
              40                      45                      50

gct cca  att  tca  agc  cga  cag  gtt  ttc  cat  gga  gtg  gtg  gaa  gat  tcc    307
Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly Val Val Glu Asp Ser
              55                      60                      65

atc tat  atc  cac  ccc  cag  ggc  caa  ggc  cga  gga  atc  ggc  ggc  gct  ttg    355
Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly Ile Gly Gly Ala Leu
              70                      75                      80                      85

ctc gac  gcc  ctt  atc  acc  tac  tgc  gaa  agc  aac  ggc  atc  tgg  tgg  atc    403

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Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn Gly Ile Trp Ser Ile
 90 95 100
 cac tcc tgg atc ttc ccg gaa aac ctc ggt tct gcg aaa ctg cat gaa 451
 His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser Ala Lys Leu His Glu
 105 110 115
 tcg aag ggc ttc gtg aag gtg ggc acc atg cac caa atg gca agg atg 499
 Ser Lys Gly Phe Val Lys Val Gly Thr Met His Gln Met Ala Arg Met
 120 125 130
 ccc tac ggc gag atg gaa gga caa tgg cgc gat tgt gat ctg tgg gag 547
 Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp Cys Asp Leu Trp Glu
 135 140 145
 tgc ctc tta tcc gtt cca gag caa gct caa agt tcc taaagcaatt 593
 Cys Leu Leu Ser Val Pro Glu Gln Ala Gln Ser Ser
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 35 40 45
 Gly Trp Val Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly
 50 55 60
 Val Val Glu Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly
 65 70 75 80
 Ile Gly Gly Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn
 85 90 95
 Gly Ile Trp Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser
 100 105 110
 Ala Lys Leu His Glu Ser Lys Gly Phe Val Lys Val Gly Thr Met His
 115 120 125
 Gln Met Ala Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp
 130 135 140
 Cys Asp Leu Trp Glu Cys Leu Leu Ser Val Pro Glu Gln Ala Gln Ser
 145 150 155 160
 Ser

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					Met	Arg	Phe	Gly	Leu							
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gac	ttg	gga	act	acc	cgc	aca	atc	gcg	gcc	gtg	gac	cgc	gga	aac	163	
Asp	Leu	Gly	Thr	Thr	Arg	Thr	Ile	Ala	Ala	Val	Asp	Arg	Gly	Asn		
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tat	ccc	atc	gtc	act	gtg	gaa	gat	tct	tta	ggc	gac	acc	cac	gat	ttc	211
Tyr	Pro	Ile	Val	Thr	Val	Glu	Asp	Ser	Leu	Gly	Asp	Thr	His	Asp	Phe	
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att	cca	tct	gtg	gtg	gcc	ctc	aag	gca	gat	agg	att	gtc	gcg	ggt	tgg	259
Ile	Pro	Ser	Val	Val	Ala	Leu	Lys	Ala	Asp	Arg	Ile	Val	Ala	Gly	Trp	
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gat	gct	att	gag	gtt	ggg	cag	gac	cac	cct	tcc	ttc	gta	cgt	tct	ttc	307
Asp	Ala	Ile	Glu	Val	Gly	Gln	Asp	His	Pro	Ser	Phe	Val	Arg	Ser	Phe	
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aaa	cgc	cta	ctc	tct	gaa	ccc	aat	gtc	acg	gaa	gcc	acc	ccg	gtc	tac	355
Lys	Arg	Leu	Leu	Ser	Glu	Pro	Asn	Val	Thr	Glu	Ala	Thr	Pro	Val	Tyr	
	70				75					80					85	
ttg	ggc	gat	cat	gta	cac	cct	ttg	ggc	gcc	gtc	ctg	gag	gct	ttt	gcg	403
Leu	Gly	Asp	His	Val	His	Pro	Leu	Gly	Ala	Val	Leu	Glu	Ala	Phe	Ala	
				90					95					100		
gaa	aac	gtg	gtc	act	gcg	ctg	cgt	gca	ttt	cag	acg	caa	ttg	gga	gat	451
Glu	Asn	Val	Val	Thr	Ala	Leu	Arg	Ala	Phe	Gln	Thr	Gln	Leu	Gly	Asp	
				105				110					115			
acc	tcc	ccg	atc	gaa	gta	gtc	att	ggg	gtg	ccc	gcc	aac	tcc	cac	agc	499
Thr	Ser	Pro	Ile	Glu	Val	Val	Ile	Gly	Val	Pro	Ala	Asn	Ser	His	Ser	
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Val	Val	Gly	Leu	Val	Asn	Glu	Pro	Ser	Ala	Ala	Ala	Phe	Glu	Tyr	Thr	
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 Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr
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Asp	Asp	Leu	Asp	Leu	Ala	Glu	Gln	His	Gly	Asp	Leu	Asn	Glu	Gly	Pro
			130			135					140				
Leu	Lys	Ser	Leu	Ser	Asp	Lys	Leu	Ile	Asn	Ile	Leu	Gly	Gly	Leu	Lys
					150					155					160
Val	Glu	Ser	Phe	Gly	Glu	Ile	Gly	Glu	Ala	Phe	Asp	Pro	Glu	Ile	His
			165					170						175	
Glu	Ala	Val	Gln	Asp	Leu	Ser	Gln	Gly	Asp	Val	Lys	Val	Leu	Gly	Thr
			180					185					190		
Val	Leu	Arg	Lys	Gly	Tyr	Arg	Leu	Gly	Asp	Arg	Val	Ile	Arg	Thr	Ala
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Met	Val	Leu	Ile	Gly	Asp	Pro	Glu	Glu	Ser						
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<210> 31
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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1954)  
<223> RXN02543
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gga att gac ctt gga acc acc aac tct gtg gtt tcc gta ctt gaa ggc		163
Gly Ile Asp Leu	Gly Thr Thr Asn Ser Val Val Ser Val Leu	Glu Gly
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ggc gag cca gta gtt atc gca aac gca gaa ggc tca cgc acc acc cct		211
Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly Ser Arg Thr Thr Pro		
	25 30 35	
tcc gtc gtt gca ttc gca aag aac ggt gaa gtt cta gtc ggc cag tcc		259
Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val Leu Val Gly Gln Ser		
	40 45 50	
gct aag aac cag cgc gtc acc aac gtt gac cgc acc att cgc tcc gtc		307
Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg Thr Ile Arg Ser Val		
	55 60 65	

090303-062000

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 Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala Ile Asp Asp Lys Asn 85
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 Tyr Thr Ser Gln Ala Ile Ser Ala Arg Thr Leu Met Lys Leu Lys Arg 100
 90 95

gac gct gaa gca tac ctg ggc gag gac gtc act gat gct gtt att acc 451
 Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr Asp Ala Val Ile Thr 115
 105 110

gtt cct gca tac ttc gag gac tca cag cgc cag gca acc aag gaa gct 499
 Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln Ala Thr Lys Glu Ala 130
 120 125

ggt cag atc gca ggc ctt aac gtt ctg cgt att gtt aac gag cca acc 547
 Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile Val Asn Glu Pro Thr 145
 135 140

gcg gct gca ctt gca tac ggc ctt gag aag ggc gag cag gag cag acc 595
 Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly Glu Gln Glu Gln Thr 165
 150 155 160

att ctg gta ttc gac ctc ggt ggc ggc acc ttc gac gtc tcc ctc cta 643
 Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu 180
 170 175

gag atc ggc gac ggt gtt gtt gag gtt cgc gca acc tcc ggc gat aac 691
 Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala Thr Ser Gly Asp Asn 195
 185 190

gag ctc ggt ggc gac gac tgg gat cag cgt atc gtt gac tgg ctg gta 739
 Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile Val Asp Trp Leu Val 210
 200 205

gag aag ttc cag tcc tcc aac ggc att gac ctg acc aag gac aag atg 787
 Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu Thr Lys Asp Lys Met 225
 215 220

gcc ctg cag cgt ctg cgt gag gca gct gag aag gca aag atc gag ctg 835
 Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu 245
 230 235 240

tcc tct tcc cag agt gca aac atc aac ctt cct tac atc acc gtt gat 883
 Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro Tyr Ile Thr Val Asp 260
 250 255

gca gac aag aac cca ctg ttc ttg gat gag acc ctt tcc cgt gcc gag 931
 Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr Leu Ser Arg Ala Glu 275
 265 270

ttc cag cgc atc acc cag gac ctc ctg gcc cgc acc aag act cct ttc 979
 Phe Gln Arg Ile Thr Gln Asp Leu Leu Ala Arg Thr Lys Thr Pro Phe 290
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aac cag gtt gtt aag gac gct ggc gtg tcc gtc tcg gag atc gac cac 1027
 Asn Gln Val Val Lys Asp Ala Gly Val Ser Val Ser Glu Ile Asp His 305
 295 300

gtt gtt ctc gtc ggt ggt tcc acc cgt atg cct gct gtt acc gaa ctg 1075

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Val Val Leu Val Gly Gly Ser Thr Arg Met Pro Ala Val Thr Glu Leu
 310 315 320 325
 gtc aag gaa ctg acc ggt gga cgt gag cca aac aag ggt gtt aac cca 1123
 Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn Lys Gly Val Asn Pro
 330 335 340
 gat gag gtt gtt gca gtt ggt gca gca ctt cag gcc ggt gtt ctc cgc 1171
 Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln Ala Gly Val Leu Arg
 345 350 355
 ggc gag gtc aag gat gtt ctt ctt ctt gac gtc acc cca ctg tcc ctc 1219
 Gly Glu Val Lys Asp Val Leu Leu Asp Val Thr Pro Leu Ser Leu
 360 365 370
 ggc att gag acc aag ggt ggc gtg atg acc aag ctc atc gag cgc aac 1267
 Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys Leu Ile Glu Arg Asn
 375 380 385
 acc acc atc cct acc aag cgt tcc gag acc ttc acc acc gca gag gac 1315
 Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe Thr Thr Ala Glu Asp
 390 395 400 405
 aac cag cct tct gtt cag atc cag gtc ttc cag gcc gag cgt gaa atc 1363
 Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln Gly Glu Arg Glu Ile
 410 415 420
 gca acc gcc aac aag ctg ctc gga tcc ttc gag ctc gcc ggc atc gca 1411
 Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu Leu Gly Gly Ile Ala
 425 430 435
 cct gca cca cgt ggc gtc cca cag atc gag gtc act ttc gac atc gac 1459
 Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Ile Asp
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 gcc aac gcc atc gtc cac gtc acc gca aag gac aag ggt act ggc aag 1507
 Ala Asn Gly Ile Val His Val Thr Ala Lys Asp Lys Gly Thr Gly Lys
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 Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly Leu Ser Gln Asp Glu
 470 475 480 485
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 Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His Ala Asp Glu Asp Lys
 490 495 500
 aag cgc cgc gag gag cag gaa gtc cgc aac aac gct gag tcc ctg gtt 1651
 Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn Ala Glu Ser Leu Val
 505 510 515
 tac cag acc cgc aag ttc gtt gaa gag aac tcc gag aag gtc tcc gaa 1699
 Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser Glu Lys Val Ser Glu
 520 525 530
 gac ctc aag gca aag gtc gaa gag gca gcc aag gcc gtt gaa gaa gca 1747
 Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys Gly Val Glu Glu Ala
 535 540 545
 ctc aag gcc gag gac ctc gag gca atc aag gct gca gtt gag aag ctg 1795
 Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala Ala Val Glu Lys Leu

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550		555		560		565	
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Asn Thr Glu Ser	Gln Glu Met Gly Lys	Ala Ile Tyr Glu Ala	Asp Ala				
	570	575	580				
gct gct ggt gca acc cag gct gac gca ggt gca gaa ggc	gct gca gat	1891					
Ala Ala Gly Ala	Thr Gln Ala Asp Ala	Gly Ala Glu Gly Ala Ala Asp					
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gac aat gtt gtt gac gct gaa gtt gtc gaa gac gac gca gct gac aat	1939						
Asp Asn Val Val Asp Ala Glu Val Val Glu Asp Asp Ala Ala Asp Asn							
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Ser	Arg	Thr	Thr	Pro	Ser	Val	Val	Ala	Phe	Ala	Lys	Asn	Gly	Glu	Val
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Leu	Val	Gly	Gln	Ser	Ala	Lys	Asn	Gln	Ala	Val	Thr	Asn	Val	Asp	Arg
	50					55						60			
Thr	Ile	Arg	Ser	Val	Lys	Arg	His	Ile	Gly	Thr	Asp	Trp	Ser	Val	Ala
	65				70					75					80
Ile	Asp	Asp	Lys	Asn	Tyr	Thr	Ser	Gln	Glu	Ile	Ser	Ala	Arg	Thr	Leu
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Met	Lys	Leu	Lys	Arg	Asp	Ala	Glu	Ala	Tyr	Leu	Gly	Glu	Asp	Val	Thr
			100					105					110		
Asp	Ala	Val	Ile	Thr	Val	Pro	Ala	Tyr	Phe	Glu	Asp	Ser	Gln	Arg	Gln
							120					125			
Ala	Thr	Lys	Glu	Ala	Gly	Gln	Ile	Ala	Gly	Leu	Asn	Val	Leu	Arg	Ile
	130					135					140				
Val	Asn	Glu	Pro	Thr	Ala	Ala	Ala	Leu	Ala	Tyr	Gly	Leu	Glu	Lys	Gly
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Glu	Gln	Glu	Gln	Thr	Ile	Leu	Val	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe
				165					170					175	
Asp	Val	Ser	Leu	Leu	Glu	Ile	Gly	Asp	Gly	Val	Val	Glu	Val	Arg	Ala
			180					185					190		

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 Val Asp Trp Leu Val Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu
 210 215 220
 Thr Lys Asp Lys Met Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys
 225 230 235 240
 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro
 245 250 255
 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr
 260 265 270
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 Thr Lys Thr Pro Phe Asn Gln Val Val Lys Asp Ala Gly Val Ser Val
 290 295 300
 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
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 Ala Val Thr Glu Leu Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn
 325 330 335
 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
 340 345 350
 Ala Gly Val Leu Arg Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
 355 360 365
 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys
 370 375 380
 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
 385 390 395 400
 Thr Thr Ala Glu Asp Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln
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 Gly Glu Arg Glu Ile Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu
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 Leu Gly Gly Ile Ala Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val
 435 440 445
 Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp
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 465 470 475 480
 Leu Ser Gln Asp Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His
 485 490 495
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 500 505 510
 Ala Glu Ser Leu Val Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser

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530	535	540
Gly Val Glu Glu Ala Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala		
545	550	555
Ala Val Glu Lys Leu Asn Thr Glu Ser Gln Glu Met Gly Lys Ala Ile		
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Tyr Glu Ala Asp Ala Ala Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala		
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Glu Gly Ala Ala Asp Asp Asn Val Val Asp Ala Glu Val Val Glu Asp		
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 <223> FRXA02543

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 Met Gly Arg Ala Val
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gga att gac ctt gga acc acc aac tct gtg gtt tcc gta ctt gaa ggc 163
 Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val Ser Val Leu Glu Gly
 10 15 20

ggc gag cca gta gtt atc gca aac gca gaa ggc tca cgc acc acc cct 211
 Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly Ser Arg Thr Thr Pro
 25 30 35

tcc gtc gtt gca ttc gca aag aac ggt gaa gtt cta gtc ggc cag tcc 259
 Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val Leu Val Gly Gln Ser
 40 45 50

gct aag aac cag cgc gtc acc aac gtt gac cgc acc att cgc tcc gtc 307
 Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg Thr Ile Arg Ser Val
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aag cgc cac atc ggc acc gac tgg tcc gtt gct atc gat gac aag aac 355
 Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala Ile Asp Asp Lys Asn
 70 75 80 85

tac acc tca cag gaa atc tcg gct cgt acc ctg atg aag ctg aag cgc 403
 Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu Met Lys Leu Lys Arg
 90 95 100

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gcg gct gca ctt gca tac ggc ctt gag aag ggc gag gag gag acc Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly Glu Gln Glu Gln Thr	595
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gag atc ggc gac ggt gtt gtt gag gtt cgc gca acc tcc ggc gat aac Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala Thr Ser Gly Asp Asn	691
gag ctc ggt ggc gac gac tgg gat cag cgt atc gtt gac tgg ctg gta Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile Val Asp Trp Leu Val	739
gag aag ttc cag tcc tcc aac ggc att gac ctg acc aag gac aag atg Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu Thr Lys Asp Lys Met	787
gcc ctg cag cgt ctg cgt gag gca gct gag aag gca aag atc gag ctg Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu	835
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aac cag gtt gtt aag gac gct ggc gtg tcc gtc tcg gag atc gac cac Asn Gln Val Val Lys Asp Ala Gly Val Ser Val Ser Glu Ile Asp His	1027
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 Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val Thr Pro Leu Ser Leu
 360 365 370

ggc att gag acc aag ggt ggc gtg atg acc aag ctc atc gag cgc aac 1267
 Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys Leu Ile Glu Arg Asn
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acc acc atc cct acc aag cgt tcc gag acc ttc acc acc gca gag gac 1315
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gca acc gcc aac aag ctg ctc gga tcc ttc gag ctc gcc gcc atc gca 1411
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 425 430 435

cct gca cca cgt ggc gtc cca cag atc gag gtc act ttc gac atc gac 1459
 Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Ile Asp
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 490 495 500

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 Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn Ala Glu Ser Leu Val
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 Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser Glu Lys Val Ser Glu
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 50 55 60
 Thr Ile Arg Ser Val Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala
 65 70 75 80
 Ile Asp Asp Lys Asn Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu
 85 90 95
 Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr
 100 105 110
 Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln
 115 120 125
 Ala Thr Lys Glu Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
 130 135 140
 Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly
 145 150 155 160
 Glu Gln Glu Gln Thr Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
 165 170 175
 Asp Val Ser Leu Leu Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala
 180 185 190
 Thr Ser Gly Asp Asn Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile
 195 200 205
 Val Asp Trp Leu Val Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu
 210 215 220
 Thr Lys Asp Lys Met Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys

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Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr	260	265	270
Leu Ser Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Ala Arg	275	280	285
Thr Lys Thr Pro Phe Asn Gln Val Val Lys Asp Ala Gly Val Ser Val	290	295	300
Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro	305	310	315
Ala Val Thr Glu Leu Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn	325	330	335
Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln	340	345	350
Ala Gly Val Leu Arg Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val	355	360	365
Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys	370	375	380
Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe	385	390	395
Thr Thr Ala Glu Asp Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln	405	410	415
Gly Glu Arg Glu Ile Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu	420	425	430
Leu Gly Gly Ile Ala Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val	435	440	445
Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp	450	455	460
Lys Gly Thr Gly Lys Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly	465	470	475
Leu Ser Gln Asp Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His	485	490	495
Ala Asp Glu Asp Lys Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn	500	505	510
Ala Glu Ser Leu Val Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser	515	520	525
Glu Lys Val Ser Glu Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys	530	535	540
Gly Val Glu Glu Ala Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala	545	550	555
			560

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Ala Val Glu Lys Leu Asn Thr Glu Ser Gln Glu Met Gly Lys Xaa Ile
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Xaa Glu Ala Asp Ala Xaa Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala
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Glu Gly Ala Ala Asp Asp Asn Val Val Asp Ala Glu Val Val Glu Asp
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Asp Ala Ala Asp Asn Gly Glu Asp Lys Lys
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<222> {101}..{1924}

<223> RXN02280

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Met Gln Glu Ser Ser
1 5

cgt gat aat ttc caa gtt gac ctc ggc ggc gtt gtt gat ctt ttg agt 163
Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val Val Asp Leu Leu Ser
10 15 20

cgc cac att tat tcc ggt cgg agg gtg tat gtg cgt gag ttg ctg cag 211
Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val Arg Glu Leu Leu Gln
25 30 35

aat gcg gtt gat gct tgt act gca cgt tct gaa cag ggt gag gag ggc 259
Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu Gln Gly Glu Glu Gly
40 45 50

tac gag ccg agt att cgt att cgg ccg gtg acc aag gat cgt gcc acg 307
Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr Lys Asp Arg Ala Thr
55 60 65

ttt tca ctg gtt gat aat ggt acg ggc ctg acc gcg cag gag gcg cgg 355
Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr Ala Gln Glu Ala Arg
70 75 80 85

gaa ttg ctg gcg acg gtg ggg cgg acg tcg aaa cgc gat gaa ttc ggt 403
Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys Arg Asp Glu Phe Gly
90 95 100

ctg cag cgg gaa ggt cgc ctg ggg caa ttt ggc atc ggg ctg ctt agt 451
Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly Ile Gly Leu Leu Ser
105 110 115

tgt ttc atg gtg gcg gat gag atc acc atg gtg tcg cat gcg gag ggt 499
Cys Phe Met Val Ala Asp Glu Ile Thr Met Val Ser His Ala Glu Gly

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120	125	130	
gcg tcg gcg att cgg tgg act ggt cat gcg gat ggc acc ttt aac ctg			547
Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp Gly Thr Phe Asn Leu			
135	140	145	
gag att ctt ggg gat gac gca acg gat gtc att ccg gtg ggc acg act			595
Glu Ile Leu Gly Asp Ala Thr Asp Val Ile Pro Val Gly Thr Thr			
150	155	160	165
gtg cac ctg act ccg cgc cct gat gag cgc acg ttg ctg acg gaa aat			643
Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr Leu Leu Thr Glu Asn			
170	175	180	
tcc gtg gtc acc att gct agt aat tat ggc cgc tac ctg ccg att cct			691
Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg Tyr Leu Pro Ile Pro			
185	190	195	
att gtg gtg cag ggt gag aaa aac acc acc atc act aca tcg ccg gtg			739
Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile Thr Ser Pro Val			
200	205	210	
ttt gca aag gat act gat cag cag cac agg ctg tat gcc ggc ccg gag			787
Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu Tyr Ala Gly Arg Glu			
215	220	225	
cgc ctt ggt aaa act cct ttt gat gtc atc gat ctc acc ggt cct ggc			835
Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp Leu Thr Gly Pro Gly			
230	235	240	245
atc gag ggt gtg gct tat gta ttg ccg gag gcc cag gct ccg cat atg			883
Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala Gln Ala Pro His Met			
250	255	260	
tcc agg cgt cac agt att tat gtc aac cgc atg ttg gtc tct gat ggg			931
Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met Leu Val Ser Asp Gly			
265	270	275	
cct tcc acg gtg ctg ccc aac tgg gcg ttc ttt gtg gaa tgt gaa atc			979
Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe Val Glu Cys Glu Ile			
280	285	290	
aat tca acc gat ttg gaa ccc acc gca tcg cgt gaa gcg ctc atg gat			1027
Asn Ser Thr Asp Leu Glu Pro Thr Ala Ser Arg Glu Ala Leu Met Asp			
295	300	305	
gac acc gcg ttc gcg gca acc agg gaa cat atc ggt gag tgc att aaa			1075
Asp Thr Ala Phe Ala Ala Thr Arg Glu His Ile Gly Glu Cys Ile Lys			
310	315	320	325
tcg tgg ctg att aat ctc gcc atg acc aag cct cac cgc gtg ccg gaa			1123
Ser Trp Leu Ile Asn Leu Ala Met Thr Lys Pro His Arg Val Arg Glu			
330	335	340	
ttt act gcg att cat gat ctt gcc ctg cgc gag ctg tgc caa tcg gac			1171
Phe Thr Ala Ile His Asp Leu Ala Leu Arg Glu Leu Cys Gln Ser Asp			
345	350	355	
gcg gac ctg gct gaa acc atg ttg ggt ctt ctc acc ttg gag acc tcc			1219
Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu Thr Leu Glu Thr Ser			
360	365	370	

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cgt ggt cgc atc tcg atc ggt gag atc acc acg ttg tcc atc acc gag 1267
 Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu
 375 380 385

gat gtg tcg ctg cag ctg gct acc acg ttg gat gat ttc agg cag ctc 1315
 Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu
 390 395 400 405

aac acc att gcg cgc ccg gac acc ttg att att aat ggc ggc tac att 1363
 Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Pro Ile
 410 415 420

cac gac agc gat ctg gct cgg ctc att ccc gtt cac tac cca ccg ctt 1411
 His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu
 425 430 435

acg gta tct act gct gac ctg cgc gaa tcc atg gat ctg atg gag ctt 1459
 Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu
 440 445 450

ccg ccg ctg cag gac att gag aaa gcc aag gca ctg gat gcg cag gtc 1507
 Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val
 455 460 465

acg gaa tca ttg aag gat ttt cag atc aag ggc gca acg agg gtt ttt 1555
 Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe
 470 475 480 485

gaa ccc gca gat gtt cct gcc gtg gtg atc att gat tcc aag gcg cag 1603
 Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln
 490 495 500

gcc tca cgg gat cgc aat gaa aca caa agc gca acc act gat cgt tgg 1651
 Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp
 505 510 515

gct gac att ttg gca acg gtg gat aac acg ttg agc cgt caa aca gcc 1699
 Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala
 520 525 530

aac att cca cag gat cag gga ctg tcg gcg ttg tgc ttg aat tgg aac 1747
 Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn
 535 540 545

aat tcg ctg gtc agg aaa ttg gcg tcc act gat gac acc gcc gtg gtg 1795
 Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val
 550 555 560 565

tcg cgc acg gtg cgt ttg ctc tac gtt cag gca ttg ttg tcc agc aag 1843
 Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys
 570 575 580

agg cca ctg ccg gtg aag gaa cgc gcg ctg ctt aat gat tcg ctg gca 1891
 Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala
 585 590 595

gat ctg gtt tct ttg tct ttg tca tcc gat atc taagacaatc ctccgctaata 1944
 Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
 600 605

006290" 8023066

ctt

1947

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 <212> PRT
 <213> Corynebacterium glutamicum

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 Val Asp Leu Leu Ser Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val
 20 25 30
 Arg Glu Leu Leu Gln Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu
 35 40 45
 Gln Gly Glu Glu Gly Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr
 50 55 60
 Lys Asp Arg Ala Thr Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr
 65 70 75 80
 Ala Gln Glu Ala Arg Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys
 85 90 95
 Arg Asp Glu Phe Gly Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly
 100 105 110
 Ile Gly Leu Leu Ser Cys Phe Met Val Ala Asp Glu Ile Thr Met Val
 115 120 125
 Ser His Ala Glu Gly Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp
 130 135 140
 Gly Thr Phe Asn Leu Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile
 145 150 155 160
 Pro Val Gly Thr Thr Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr
 165 170 175
 Leu Leu Thr Glu Asn Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg
 180 185 190
 Tyr Leu Pro Ile Pro Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile
 195 200 205
 Thr Thr Ser Pro Val Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu
 210 215 220
 Tyr Ala Gly Arg Glu Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp
 225 230 235 240
 Leu Thr Gly Pro Gly Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala
 245 250 255
 Gln Ala Pro His Met Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met
 260 265 270
 Leu Val Ser Asp Gly Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe

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0963203 " 062300

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<213> Corynebacterium glutamicum
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<223> FRXA02282
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	cgt	gat	aat	ttc	caa	ggt	gac	ctc	ggc	ggt	ggt	gat	ctt	ttg	agt	163	
	Arg	Asp	Asn	Phe	Gln	Val	Asp	Leu	Gly	Val	Val	Val	Asp	Leu	Leu	Ser	
					10									20			
	cgc	cac	att	tat	tcc	ggt	ccg	agg	gtg	tat	gtg	cgt	gag	ttg	ctg	cag	211
	Arg	His	Ile	Tyr	Ser	Gly	Pro	Arg	Val	Tyr	Val	Arg	Glu	Leu	Leu	Gln	
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	aat	cgc	ggt	gat	gct	tgt	act	gca	cgt	tct	gaa	cag	ggt	gag	gag	ggc	259
	Asn	Ala	Val	Asp	Ala	Cys	Thr	Ala	Arg	Ser	Glu	Gln	Gly	Glu	Glu	Gly	
					40			45					50				
	tac	gag	ccg	agt	att	cgt	att	cgg	ccg	gtg	acc	aag	gat	cgt	gcc	acg	307
	Tyr	Glu	Pro	Ser	Ile	Arg	Ile	Arg	Pro	Val	Thr	Lys	Asp	Arg	Ala	Thr	
		55					60					65					
	ttt	tca	ctg	ggt	gat	aat	ggt	acg	ggc	ctg	acc	gcg	cag	gag	gcg	cgg	355
	Phe	Ser	Leu	Val	Asp	Asn	Gly	Thr	Gly	Leu	Thr	Ala	Gln	Glu	Ala	Arg	
	70					75					80					85	
	gaa	ttg	ctg	gcg	acg	gtg	ggg	cgg	acg	tcg	aaa	cgc	gat	gaa	ttc	ggt	403
	Glu	Leu	Leu	Ala	Thr	Val	Gly	Arg	Thr	Ser	Lys	Arg	Asp	Glu	Phe	Gly	
					90					95					100		
	ctg	cag	cgg	gaa	ggt	cgc	ctg	ggg	caa	ttt	ggc						436
	Leu	Gln	Arg	Glu	Gly	Arg	Leu	Gly	Gln	Phe	Gly						
				105					110								

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<210> 38
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<212> PRT
<213> Corynebacterium glutamicum
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Val Asp Leu Leu Ser Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val

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Arg	Glu	Leu	Leu	Gln	Asn	Ala	Val	Asp	Ala	Cys	Thr	Ala	Arg	Ser	Glu			
		35					40						45					
Gln	Gly	Glu	Glu	Gly	Tyr	Glu	Pro	Ser	Ile	Arg	Ile	Arg	Pro	Val	Thr			
		50					55				60							
Lys	Asp	Arg	Ala	Thr	Phe	Ser	Leu	Val	Asp	Asn	Gly	Thr	Gly	Leu	Thr			
		65			70					75					80			
Ala	Gln	Glu	Ala	Arg	Glu	Leu	Leu	Ala	Thr	Val	Gly	Arg	Thr	Ser	Lys			
				85					90					95				
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<213> Corynebacterium glutamicum

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<223> RXA00886

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Val Ala Arg Asp Tyr
1 5

tac ggc att ctc ggc gtc gat cgc aat gca acc gaa tca gag atc aaa 163
Tyr Gly Ile Leu Gly Val Asp Arg Asn Ala Thr Glu Ser Glu Ile Lys
10 15 20

aag gca tac cga aag ctt gcc cgc aaa tac cac ccg gac gta aac cca 211
Lys Ala Tyr Arg Lys Leu Ala Arg Lys Tyr His Pro Asp Val Asn Pro
25 30 35

ggt gag gaa gca gcg gag aaa ttc cgc gag gct tct gtt gcg cat gag 259
Gly Glu Glu Ala Ala Glu Lys Phe Arg Glu Ala Ser Val Ala His Glu
40 45 50

gta ctc act gat ccg gat aag cgc cgc att gtt gat atg ggc ggt gac 307
Val Leu Thr Asp Pro Asp Lys Arg Arg Ile Val Asp Met Gly Gly Asp
55 60 65

cca atg gag caa ggc ggc gga gct ggc gct ggt ggc ttc ggt gga ggc 355
Pro Met Glu Gln Gly Gly Gly Ala Gly Ala Gly Phe Gly Gly Gly
70 75 80 85

ttc ggc ggc agc ggt gga ctg ggc gat atc ttc gat gcc ttc ttc ggc 403
Phe Gly Gly Ser Gly Gly Leu Gly Asp Ile Phe Asp Ala Phe Phe Gly
90 95 100

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056303-13

ggt ggc gcg ggc ggt tcc cgt gga cca cgt tcc cgc gtg cag cca ggc 451
 Gly Gly Ala Gly Gly Ser Arg Gly Pro Arg Ser Arg Val Gln Pro Gly
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agt gac acc ttg tgg cgc acc tcc atc acc ttg gaa gag gct tac aag 499
 Ser Asp Thr Leu Trp Arg Thr Ser Ile Thr Leu Glu Glu Ala Tyr Lys
 120 125 130

ggc gct aag aaa gat ctc acc ctt gac acc gca gtg ctg tgt acc aag 547
 Gly Ala Lys Lys Asp Leu Thr Leu Asp Thr Ala Val Leu Cys Thr Lys
 135 140 145

tgt cat ggt tct gga tct gca tcc gac aag aag cct gtt acc tgt ggc 595
 Cys His Gly Ser Gly Ser Ala Ser Asp Lys Lys Pro Val Thr Cys Gly
 150 155 160 165

acc tgt aat ggc gct ggt gaa att cag gaa gtg cag cgc agc ttc ctg 643
 Thr Cys Asn Gly Ala Gly Glu Ile Gln Glu Val Gln Arg Ser Phe Leu
 170 175 180

ggc aac gtc atg acg tcc cgc cca tgc cac acc tgc gat ggc acc ggt 691
 Gly Asn Val Met Thr Ser Arg Pro Cys His Thr Cys Asp Gly Thr Gly
 185 190 195

gag atc atc cca gat cct tgc act gag tgt gca gca gat ggt cgt gtg 739
 Glu Ile Ile Pro Asp Pro Cys Thr Glu Cys Ala Ala Asp Gly Arg Val
 200 205 210

cgt gct cgc cgc gac atc gtg gcc aac atc cca gct ggc atc cag tcc 787
 Arg Ala Arg Arg Asp Ile Val Ala Asn Ile Pro Ala Gly Ile Gln Ser
 215 220 225

ggc atg cgc atc cgc atg gca ggc caa ggt gag gtt ggc gct ggt ggc 835
 Gly Met Arg Ile Arg Met Ala Gly Gln Gly Glu Val Gly Ala Gly Gly
 230 235 240 245

ggt cct gcg ggt gac ctc tac att gaa gtc atg gtg cgc ccg cac gcc 883
 Gly Pro Ala Gly Asp Leu Tyr Ile Glu Val Met Val Arg Pro His Ala
 250 255 260

atc ttc acc cgc gat ggc gac gat ctg cac gcc agc atc aag gtt cca 931
 Ile Phe Thr Arg Asp Gly Asp Asp Leu His Ala Ser Ile Lys Val Pro
 265 270 275

atg ttc gat gca gcg ctt ggc acc gaa ttg gac gtg gaa tcc ctc acc 979
 Met Phe Asp Ala Ala Leu Gly Thr Glu Leu Asp Val Glu Ser Leu Thr
 280 285 290

ggc gaa gag gtg aaa att acc atc cct gca ggt act cag ccc aac gat 1027
 Gly Glu Glu Val Lys Ile Thr Ile Pro Ala Gly Thr Gln Pro Asn Asp
 295 300 305

gtg atc acc ttg gat ggt gaa ggc atg ccg aag ctg cgc gca gaa ggc 1075
 Val Ile Thr Leu Asp Gly Glu Gly Met Pro Lys Leu Arg Ala Glu Gly
 310 315 320 325

cac ggc aac ctc atg gcg cat gtc gat cta ttt gtg cca acc gat ttg 1123
 His Gly Asn Leu Met Ala His Val Asp Leu Phe Val Pro Thr Asp Leu
 330 335 340

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gat gac cgc acc cgc gaa ttg ctt gaa gaa atc cgc aac cat cgc agc 1171
 Asp Asp Arg Thr Arg Glu Leu Leu Glu Glu Ile Arg Asn His Arg Ser
 345 350 355

gac aac gct tcc gtg cat cgc gaa ggc gga gaa gaa tcc ggt ttc ttt 1219
 Asp Asn Ala Ser Val His Arg Glu Gly Gly Glu Glu Ser Gly Phe Phe
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gac aag ctc cga aac aag ttc cgc aaa taatgtcact gccagtatatt 1266
 Asp Lys Leu Arg Asn Lys Phe Arg Lys
 375 380

atc 1269

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 <213> Corynebacterium glutamicum

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Glu Ser Glu Ile Lys Lys Ala Tyr Arg Lys Leu Ala Arg Lys Tyr His
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Pro Asp Val Asn Pro Gly Glu Ala Ala Glu Lys Phe Arg Glu Ala
 35 40 45

Ser Val Ala His Glu Val Leu Thr Asp Pro Asp Lys Arg Arg Ile Val
 50 55 60

Asp Met Gly Gly Asp Pro Met Glu Gln Gly Gly Gly Ala Gly Ala Gly
 65 70 75 80

Gly Phe Gly Gly Gly Phe Gly Gly Ser Gly Gly Leu Gly Asp Ile Phe
 85 90 95

Asp Ala Phe Phe Gly Gly Gly Ala Gly Gly Ser Arg Gly Pro Arg Ser
 100 105 110

Arg Val Gln Pro Gly Ser Asp Thr Leu Trp Arg Thr Ser Ile Thr Leu
 115 120 125

Glu Glu Ala Tyr Lys Gly Ala Lys Lys Asp Leu Thr Leu Asp Thr Ala
 130 135 140

Val Leu Cys Thr Lys Cys His Gly Ser Gly Ser Ala Ser Asp Lys Lys
 145 150 155 160

Pro Val Thr Cys Gly Thr Cys Asn Gly Ala Gly Glu Ile Gln Glu Val
 165 170 175

Gln Arg Ser Phe Leu Gly Asn Val Met Thr Ser Arg Pro Cys His Thr
 180 185 190

Cys Asp Gly Thr Gly Glu Ile Ile Pro Asp Pro Cys Thr Glu Cys Ala
 195 200 205

Ala Asp Gly Arg Val Arg Ala Arg Arg Asp Ile Val Ala Asn Ile Pro

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210 215 220

Ala Gly Ile Gln Ser Gly Met Arg Ile Arg Met Ala Gly Gln Gly Glu
225 230 235 240

Val Gly Ala Gly Gly Gly Pro Ala Gly Asp Leu Tyr Ile Glu Val Met
245 250 255

Val Arg Pro His Ala Ile Phe Thr Arg Asp Gly Asp Asp Leu His Ala
260 265 270

Ser Ile Lys Val Pro Met Phe Asp Ala Ala Leu Gly Thr Glu Leu Asp
275 280 285

Val Glu Ser Leu Thr Gly Glu Glu Val Lys Ile Thr Ile Pro Ala Gly
290 295 300

Thr Gln Pro Asn Asp Val Ile Thr Leu Asp Gly Glu Gly Met Pro Lys
305 310 315 320

Leu Arg Ala Glu Gly His Gly Asn Leu Met Ala His Val Asp Leu Phe
325 330 335

Val Pro Thr Asp Leu Asp Asp Arg Thr Arg Glu Leu Leu Glu Glu Ile
340 345 350

Arg Asn His Arg Ser Asp Asn Ala Ser Val His Arg Glu Gly Gly Glu
355 360 365

Glu Ser Gly Phe Phe Asp Lys Leu Arg Asn Lys Phe Arg Lys
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<212> DNA
<213> Corynebacterium glutamicum

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<223> RXS00568

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Val Lys Ser Ser Val
1 5

gag aag ctg agc gac acc cgt tca aag atc acc gtt gag gtt cca ttt 163
Glu Lys Leu Ser Asp Thr Arg Ser Lys Ile Thr Val Glu Val Pro Phe
10 15 20

tct gaa ctg aag cca gag atc gac cag gca tac gcc gct cta gcg cag 211
Ser Glu Leu Lys Pro Glu Ile Asp Gln Ala Tyr Ala Ala Leu Ala Gln
25 30 35

caa gtc cag atc cct ggt ttc cgt aag ggc aag gca ccg cgt cag ctt 259
Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys Ala Pro Arg Gln Leu
40 45 50

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 Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu Glu Gln Val Val Asn
 55 60 65

gac atg ctt cct aac cgc tac gca cag gca atc gaa gct gag ggc atc 355
 Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile Glu Ala Glu Gly Ile
 70 75 80 85

aag gca atc ggc cag cct aac gta gag gtc acc aag atc gaa gac aac 403
 Lys Ala Ile Gly Gln Pro Asn Val Glu Val Thr Lys Ile Glu Asp Asn
 90 95 100

gag ctg gtt gag ttc gtc gct gag gtt gac gtt cgc cca gag ttc gag 451
 Glu Leu Val Glu Phe Val Ala Glu Val Asp Val Arg Pro Glu Phe Glu
 105 110 115

ctt cct aag ttc gag gac atc act gtt gag gtc cca gct atc aag gct 499
 Leu Pro Lys Phe Glu Asp Ile Thr Val Glu Val Pro Ala Ile Lys Ala
 120 125 130

gac gaa gag gca atc gaa gca gag ctg gag acc ctg cgt gca cgt ttc 547
 Asp Glu Glu Ala Ile Glu Ala Glu Leu Glu Thr Leu Arg Ala Arg Phe
 135 140 145

tcc acc ttg aag gat cac aac cac aag ctg aag aag ggt gag ttc gtc 595
 Ser Thr Leu Lys Asp His Asn His Lys Leu Lys Lys Gly Glu Phe Val
 150 155 160 165

acc atc aac atc acc gca agc att gac ggt gag aag att gaa gag gca 643
 Thr Ile Asn Ile Thr Ala Ser Ile Asp Gly Glu Lys Ile Glu Glu Ala
 170 175 180

acc act gag ggt ctg tcc tac gaa atc gga tct gac gat ctg att gac 691
 Thr Thr Glu Gly Leu Ser Tyr Glu Ile Gly Ser Asp Asp Leu Ile Asp
 185 190 195

ggc ctg gac aag gct ctg atc ggc gct aag aag gat gaa acc gta gag 739
 Gly Leu Asp Lys Ala Leu Ile Gly Ala Lys Lys Asp Glu Thr Val Glu
 200 205 210

ttc acc tct gag ctg gca aac ggc gag cac aag ggc aag gaa gct caa 787
 Phe Thr Ser Glu Leu Ala Asn Gly Glu His Lys Gly Lys Glu Ala Gln
 215 220 225

atc agc gtt gag atc acc gca acc aag cag cgc gag ctg cct gag ctg 835
 Ile Ser Val Glu Ile Thr Ala Thr Lys Gln Arg Glu Leu Pro Glu Leu
 230 235 240 245

gat gat gag ttc gca cag ctg gct tct gag ttc gac acc atc gaa gag 883
 Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe Asp Thr Ile Glu Glu
 250 255 260

ctt cgt gag tcc acc gtg tct gac gtt gag gct aag cag aag aac gag 931
 Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala Lys Gln Lys Asn Glu
 265 270 275

cag gct gct gca atc cgc gac gaa gtt ctg gct gcg gct ctt ggc gag 979
 Gln Ala Ala Ala Ile Arg Asp Glu Val Leu Ala Ala Ala Leu Gly Glu
 280 285 290

0060200-062000

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295 300 305

cag ctg cac cag ctc ctc ggc gag ctt gca cac gac gat gct gca ctg 1075
Gln Leu His Gln Leu Leu Gly Glu Leu Ala His Asp Asp Ala Ala Leu
310 315 320 325

aac tcc ctc ctt gag gct cag ggc acc act cgt gaa gag ttc gac aag 1123
Asn Ser Leu Leu Glu Ala Gln Gly Thr Arg Glu Glu Phe Asp Lys
330 335 340

aag aac gtc gaa gat gct gag aag gct gtt cgc acc cag ctg ttc ctg 1171
Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg Thr Gln Leu Phe Leu
345 350 355

gac acc ctc tct gag gtt gag gag cct gag gtt tcc cag cag gag ctc 1219
Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val Ser Gln Gln Glu Leu
360 365 370

acc gac cac atc ctg ttc acc gca cag tct tac ggc atg gac cca aac 1267
Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr Gly Met Asp Pro Asn
375 380 385

cag ttc atc ggt cag ctg cag cag tcc ggc cag atc gcg aac ctc ttc 1315
Gln Phe Ile Gly Gln Leu Gln Gln Ser Gly Gln Ile Ala Asn Leu Phe
390 395 400 405

tcc gac gtt cgc cgt ggc aag gct ctt gca cag gct atc tgc cgc gta 1363
Ser Asp Val Arg Arg Gly Lys Ala Leu Ala Gln Ala Ile Cys Arg Val
410 415 420

aac gtg aag gac tcc gag ggt aac gag atc gac cct aag gaa tac ttc 1411
Asn Val Lys Asp Ser Glu Gly Asn Glu Ile Asp Pro Lys Glu Tyr Phe
425 430 435

ggt gaa gaa gaa gta gct gag act gag tct gaa gct taaaaacttt 1457
Gly Glu Glu Glu Val Ala Glu Thr Glu Ser Glu Ala
440 445

aaagaaataa cgc 1470

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<211> 449
<212> PRT
<213> Corynebacterium glutamicum

<400> 42
Val Lys Ser Ser Val Glu Lys Leu Ser Asp Thr Arg Ser Lys Ile Thr
1 5 10 15

Val Glu Val Pro Phe Ser Glu Leu Lys Pro Glu Ile Asp Gln Ala Tyr
20 25 30

Ala Ala Leu Ala Gln Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys
35 40 45

Ala Pro Arg Gln Leu Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu
50 55 60

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096333-19370

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<210> 43
<211> 826
<212> DNA
<213> Cornebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(826)  
<223> RXN03038
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400> 43	
ggcggcaaaa caccaagtaa gccttacagt ccgacagcct catagcggat gggataagtt	60
cctaaccact tcaaatccgt taaagtgcct gttaaaaaat atg cat tca aag gaa	115
Met His Ser Lys Glu	5
gag tta aca gtg cgt aaa gga att tcc cgc gtc ctg tcg gta gcg gtt	163
Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val Leu Ser Val Ala Val	20
gct agt tca atc gga ttc gga act gta ctg aca gcc acc gcc atc gca	211
Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr Gly Thr Gly Ile Ala	35
gca gct caa gac tct gca ttt gac tac ggt atg gat cca aac atg aac	259
Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Asn Met Asn	50
tac aac ccg atc gat gac atc aag gat cgt ccc gaa gga ttg tcc aat	307
Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro Glu Gly Leu Ser Asn	65
ctt ccc tac ttc gga agt aaa ttg acc agc tgg ggc tca tca tat gcc	355
Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Tyr Ala	85
acc gcc tca tcc gcc gtc gtg acc tcc gcg ctc ccg cag tac acc gat	403
Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu Pro Gln Tyr Thr Asp	95
ccg cgc tac ccc ctc gcc aaa gac gac ctg ccc aag gca acc atc gac	451
Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr Ile Asp	115
atg gag cca gaa qtt ctt gcq cgc ctt gag cga ttc gtc gcc gtt gac	499

Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg Phe Val Gly Val Asp
120 125 130

ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg gga cgc 547
Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met Gly Arg
135 140 145

acc att cct cta gtc tgg gtt gtt cca gaa gac aac acc gtg cct ggc 595
Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp Asn Thr Val Pro Gly
150 155 160 165

cca acg gtc tac gca ctc gga ggc ggt gac ggt gga caa ggc ggc cag 643
Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gln Gly Gly Gln
170 175 180

aac tgg gtc acc cgc acc gac ctt gag gaa tta acc agt gac aac aac 691
Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu Thr Ser Asp Asn Asn
185 190 195

atc aac ctc atc atg ccg atg ctc gga tct ttt agt ttc tac tct gac 739
Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr Ser Asp
200 205 210

tgg gca cgc gaa agc caa tcc atg ggt tgt gcg caa cag tgg gaa aca 787
Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala Gln Gln Trp Glu Thr
215 220 225

ttg ctc atg cac gaa ctg cct gag ccg ctt gta gcg gcc 826
Leu Leu Met His Glu Leu Pro Glu Pro Leu Val Ala Ala
230 235 240

<210> 44
<211> 242
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 44
Met His Ser Lys Glu Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val
1 5 10 15

Leu Ser Val Ala Val Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr
20 25 30

Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met
35 40 45

Asp Pro Asn Met Asn Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro
50 55 60

Glu Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp
65 70 75 80

Gly Ser Ser Tyr Ala Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu
85 90 95

Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro
100 105 110

Lys Ala Thr Ile Asp Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg
115 120 125

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Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser
130 135 140

Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp
145 150 155 160

Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly
165 170 175

Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu
180 185 190

Thr Ser Asp Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe
195 200 205

Ser Phe Tyr Ser Asp Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala
210 215 220

Gln Gln Trp Glu Thr Leu Leu Met His Glu Leu Pro Glu Pro Leu Val
225 230 235 240

Ala Ala

<210> 45

<211> 653

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(630)

<223> RXN03039

<400> 45

gca ctc ccg caa tac acc gac cca cgc tac ccc ctc ggc aaa gac gac 48
Ala Leu Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp
1 5 10 15

ctg ccc aaa gca acc atc gac atg gag cca gaa gct ctt gcg cgc ctt 96
Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu
20 25 30

gag cga ttc gtc ggc gtt gac ggt gat cgc atc cgc caa atc aac gcg 144
Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala
35 40 45

tac tcg cca tca atg gga cgc acc att cct cta gtc tgg gtc gtg cca 192
Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro
50 55 60

gaa gac aac acc gtg cct ggc cca acg gtc tac gca ctc ggc ggc ggc 240
Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly
65 70 75 80

gac ggt ggc caa ggc ggc caa aac tgg gtc acc cgc acc gac ctt gat 288
Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp
85 90 95

006603206.062200

gag ttg acc agt gaa aac aac atc aac ctc atc atg ccc atg ctc gga 336
 Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly
 100 105 110

tct ttt agt ttc tac gct gac tgg gca ggc gaa agc gaa tcc atg ggt 384
 Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly
 115 120 125

ggt gcg caa cag tgg gaa aca ttc ctc atg cac gaa ctr ccm gag ccg 432
 Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro
 130 135 140

cta gaa gcg gcc atc ggc gca gac ggg caa cgc agc atc gtc ggc atg 480
 Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met
 145 150 155 160

tcc atg tcc ggg gga tcr gtg ctg aac ttt gcg acg cat gac ccc aac 528
 Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn
 165 170 175

ttt tay tcc tck gtc ggc tca ttt tct gga tgt gcc gaa acc aac tcc 576
 Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser
 180 185 190

tgg atg ggr cgc cgn tgg cat cgc agc cac tgc cta caa cgg caa tgt 624
 Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Arg Gln Cys
 195 200 205

cgt gcc tgagcaaatc ttggtgaag tag 653
 Arg Ala
 210

<210> 46
 <211> 210
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 46
 Ala Leu Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp
 1 5 10 15

Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu
 20 25 30

Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala
 35 40 45

Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro
 50 55 60

Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly
 65 70 75 80

Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp
 85 90 95

Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly
 100 105 110

Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly

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115	120	125
Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro		
130	135	140
Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met		
145	150	155
Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn		
165	170	175
Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser		
180	185	190
Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys		
195	200	205
Arg Ala		
210		

<210> 47
 <211> 432
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(409)
 <223> RXN03040

<400> 47
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 ctctacatct tcgccggttc cgggtgtgttc tctgaactag atg tca tnc ggt gac 115
 Met Ser Xaa Gly Asp
 1 5
 aac gca ccg att gat gag gat gcg ttc aaa aac cgc gtc ttg gtt ggg 163
 Asn Ala Pro Ile Asp Glu Asp Ala Phe Lys Asn Arg Val Leu Val Gly
 10 15 20
 ttt gaa atc gaa gct atg tcc aac acc tgc acc cat aac ctc aag gct 211
 Phe Glu Ile Glu Ala Met Ser Asn Thr Cys Thr His Asn Leu Lys Ala
 25 30 35
 gcg acc gat caa atg ggc atc gac aac atc aac tac gat ttc cga cca 259
 Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn Tyr Asp Phe Arg Pro
 40 45 50
 acc gga acc cac gcc tgg gat tac tgg aac gaa gcg ctc cac cgc ttc 307
 Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu Ala Leu His Arg Phe
 55 60 65
 ttc ccg ttg atg atg cag gcc ttc gcc ctc gac ggt ggt ccc atc ccg 355
 Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp Gly Gly Pro Ile Pro
 70 75 80 85
 atc tat aac cct aac ggt gtg acc tcc agc gag tct tct ntc aga act 403
 Ile Tyr Asn Pro Asn Gly Val Thr Ser Ser Glu Ser Ser Xaa Arg Thr
 90 95 100

00603200 002300 002300

gtc ttc tgatgtgagc cttggcacen gtg
Val Phe

432

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<210> 48
<211> 103
<212> PRT
<213> Corynebacterium glutamicum
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<400> 48
Met Ser Xaa Gly Asp Asn Ala Pro Ile Asp Glu Asp Ala Phe Lys Asn
1 5 10 15

Arg Val Leu Val Gly Phe Glu Ile Glu Ala Met Ser Asn Thr Cys Thr
20 25 30

His Asn Leu Lys Ala Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn
35 40 45

Tyr Asp Phe Arg Pro Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu
50 55 60

Ala Leu His Arg Phe Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp
65 70 75 80

Gly Gly Pro Ile Pro Ile Tyr Asn Pro Asn Gly Val Thr Ser Ser Glu
85 90 95

Ser Ser Xaa Arg Thr Val Phe
100

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<210> 49
<211> 835
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(835)
<223> RXN03051
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<400> 49
acatccaqaa gtagtcgttg agtatcacga gcaagtcaac gatagtaaag ataatgtcga 60

ggaactcccg ctgcctaagc gggacatagt tgcaggggac atg cgt tca gat gtt 115
Met Arg Ser Asp Val
1 5

atc gag tta ccg gag ggg gta agc aag gag aaa gct gac cag cta gaa 163
Ile Glu Leu Pro Glu Gly Val Ser Lys Glu Lys Ala Asp Gln Leu Glu
10 15 20

ggt gcg gaa gcg cga ctt aac gag ggt gca cga ctg atg gca acc acc 211
Val Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg Leu Met Ala Thr Thr
25 30 35

ggg tgt gag gtt atg tgg cca acg ggc ttc tca gtt tgt ggc cga att 259
Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile

40 45 50
 ctt gac acc tat cgc cag gtt gga ggt cag ttg tca tgg ctt ggg cca 307
 Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu Ser Trp Leu Gly Pro
 55 60 65
 ccg aag tca aac gag ttg acc aat ccc gac ggt gtt ggc aaa aga agt 355
 Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly Val Gly Lys Arg Ser
 70 75 80 85
 gaa ttt ttt ggt gga gcc atc tat tgg cac cca gac aca ggc gct tat 403
 Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr
 90 95 100
 gca gtg acc ttg gac ggt ttg cga cag tgg ggg acc ttg aac tgg gaa 451
 Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu
 105 110 115
 tca ggg cca ttg ggg tac cca acc tct ggt ccg atg gat aca aac tat 499
 Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr
 120 125 130
 ccc ctt act cag cga cag act ttt caa ggt ggt gac aac tac tac aac 547
 Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly Asp Asn Tyr Tyr Asn
 135 140 145
 cca ttg act ggc ggt gct gtg tgg ggc gat att aaa cag cgc tac gaa 595
 Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile Lys Gln Arg Tyr Glu
 150 155 160 165
 gaa ctt ggc ggc tcg aat cat gcc att ggc atc ccg atc act aat gag 643
 Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile Pro Ile Thr Asn Glu
 170 175 180
 cta cct agc ggt act gag tat ttt tac aat aat ttc tcc aat gga aca 691
 Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn Phe Ser Asn Gly Thr
 185 190 195
 att tcg tgg cga aat gat cgt cag aca cgg ttt atg tat ttg gct acg 739
 Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe Met Tyr Leu Ala Thr
 200 205 210
 cag cgg gtg tgg gat gcg ttg ggt cgg gag acg ggt cgt tta ggt ttt 787
 Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe
 215 220 225
 cct gaa gca gat gaa aca cct gag gtt tct ggt cta ttc cat gtg gcg 835
 Pro Glu Ala Asp Glu Thr Pro Glu Val Ser Gly Leu Phe His Val Ala
 230 235 240 245
 <210> 50
 <211> 245
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 50
 Met Arg Ser Asp Val Ile Glu Leu Pro Glu Gly Val Ser Lys Glu Lys
 1 5 10 15
 Ala Asp Gln Leu Glu Val Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg

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20 25 30
 Leu Met Ala Thr Thr Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser
 35 40 45
 Val Cys Gly Arg Ile Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu
 50 55 60
 Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly
 65 70 75 80
 Val Gly Lys Arg Ser Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro
 85 90 95
 Asp Thr Gly Ala Tyr Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly
 100 105 110
 Thr Leu Asn Trp Glu Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro
 115 120 125
 Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly
 130 135 140
 Asp Asn Tyr Tyr Asn Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile
 145 150 155 160
 Lys Gln Arg Tyr Glu Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile
 165 170 175
 Pro Ile Thr Asn Glu Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn
 180 185 190
 Phe Ser Asn Gly Thr Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe
 195 200 205
 Met Tyr Leu Ala Thr Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr
 210 215 220
 Gly Arg Leu Gly Phe Pro Glu Ala Asp Glu Thr Pro Glu Val Ser Gly
 225 230 235 240
 Leu Phe His Val Ala
 245

 <210> 51
 <211> 1704
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1681)
 <223> RXN03054

 <400> 51
 ggtggaaata cgcgcaaac aattttatc acagaactta tgattttttc gggttaggg 60
 cagtttgttc acatcaacta gtaacgaaag gatcatgtga atg aaa ctg ttt tcc 115
 Met Lys Leu Phe Ser
 1 5

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aag gct gca ggc gtc att gct gca gca ctt ctt gtt gca ggt ggt ata 163
 Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu Val Ala Gly Gly Ile
 10 15 20

gca cct gtg gca cag ggg caa gct agt cag gtg gtc aca cct gaa gac 211
 Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val Val Thr Pro Glu Asp
 25 30 35

caa gat gcg tat gtt caa cag ttc cac cac gaa ggg aat acc cca cct 259
 Gln Asp Ala Tyr Val Gln Gln Phe His His Glu Gly Asn Thr Pro Pro
 40 45 50

gtg gta gac ggg gtg ggt ggc tac act gag caa gaa atc gcc gag atc 307
 Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Ile Ala Glu Ile
 55 60 65

cac gag gct atc cga caa gcc caa gaa tct ggc gca cct aat gaa gag 355
 His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly Ala Pro Asn Glu Glu
 70 75 80 85

ctc att ccg ggt gag atg tgg tca gat aag gtg gag ctg cca gta act 403
 Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Val Thr
 90 95 100

att gat aaa gca gcc gct gat gag gca gag ata gct att gca cag caa 451
 Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln
 105 110 115

caa tct cag cca cag acg cga ggc ctt gct gcg gct gcg gcg tgt cag 499
 Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala Ala Ala Cys Gln
 120 125 130

acg ttt tgg ccg tca cct cat cag gtt tgt ggt gct att tta gag cgc 547
 Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly Ala Ile Leu Glu Arg
 135 140 145

tat att cag cag ggt gcc cag ttt ggg tgg atg ttg ttt ccg agt gaa 595
 Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Phe Pro Ser Glu
 150 155 160 165

ggc caa acg tta aat cct gat ggt cag ggg tat cgt cag cgg ttt atg 643
 Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met
 170 175 180

aat ggg ttt gtt tat tgg cat ccg aca act ggt gcg cat gct gtt aat 691
 Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly Ala His Ala Val Asn
 185 190 195

aat tac agt gcg cag gtg tgg gag cgt aat ggg tgg gag tct ggg tgg 739
 Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp
 200 205 210

atg ggt tat ccc act ggt ggt gaa gtc cct gtg aat ggt tcc aat ccg 787
 Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Asn Gly Ser Asn Pro
 215 220 225

att gat ggt gag ttg agt ggg tgg gtg caa act ttc caa ggt ggg cga 835
 Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg
 230 235 240 245

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gtg tat cgc agt ccg gta ttg gac ggt ttc cag gtg gcc agt att aat	883
Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln Val Ala Ser Ile Asn	
250 255 260	
ggg ctg atc ttg gat aaa tgg ctt gaa ttg ggt ggt cct gat agt gac	931
Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp	
265 270 275	
ctt ggt ttt ccc att gcg gat gag gct gtg aca gct gac ggt gtg ggt	979
Leu Gly Phe Pro Ile Ala Asp gag Ala Val Thr Ala Asp Gly Val Gly	
280 285 290	
aga ttt tct gtt ttc cag aac gga gtt gtc tac tgg cat ccg caa cac	1027
Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr Trp His Pro Gln His	
295 300 305	
gga gct cac cct ata tta ggg aat ata tac agt atc tgg aga gaa gaa	1075
Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser Ile Trp Arg Glu Glu	
310 315 320 325	
gga gct gag agt ggg gaa ttc ggt tac cct atc gcc gat cca gaa aag	1123
Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile Gly Asp Pro Glu Lys	
330 335 340	
tat aca gaa aac atg gct aat cag gta ttc gaa aaa gcc gaa ctt gca	1171
Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu Lys Gly Glu Leu Ala	
345 350 355	
gct aac cta tac ccc aat cct ctt gag gct ttt att gag ttt tta ccc	1219
Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe Ile Glu Phe Leu Pro	
360 365 370	
ttt gct aat ctt gag gaa gca ata gag tat ttt gag aac gga ttg tca	1267
Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe Glu Asn Gly Leu Ser	
375 380 385	
aat tct cgt gta gag gcg aat tca ctt aac gcc aag aaa gat tcg att	1315
Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala Lys Lys Asp Ser Ile	
390 395 400 405	
caa tgt caa tcg caa tcc gct aac att cat gtg aga acg aag agt gac	1363
Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val Arg Thr Lys Ser Asp	
410 415 420	
gga gtc ggg att agg gtt cca aag att ggg ttt aag gct agg atg gat	1411
Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp	
425 430 435	
tgc gac ctt cct gga act gtc tca gat gta gtg ggg tat gga tgg att	1459
Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val Gly Tyr Gly Trp Ile	
440 445 450	
tac tac gac tat tgg gga cga tgg gct caa gca gca tat gca caa caa	1507
Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala Ala Tyr Ala Gln Gln	
455 460 465	
ttc ttc ggt aat agg aat tct gtt gtg caa acc aat tta gag gcg ggt	1555
Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly	
470 475 480 485	
tgc agc ggg gag aag aat aca tta ttt tgg ggt act tca tat ttt cag	1603

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Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln
 490 495 500
 gtg act tat gaa ggt cag ccg tat ttc ggt cag tca gca act aat tac 1651
 Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr
 505 510 515
 gct tat ctt ccg tgt acg ata gac cgt agt taacataagg aatggaatag 1701
 Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser
 520 525
 gag 1704

 <210> 52
 <211> 527
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 52
 Met Lys Leu Phe Ser Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu
 1 5 10 15
 Val Ala Gly Gly Ile Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val
 20 25 30
 Val Thr Pro Glu Asp Gln Asp Ala Tyr Val Gln Gln Phe His His Glu
 35 40 45
 Gly Asn Thr Pro Pro Val Val Asp Gly Val Gly Tyr Thr Glu Gln
 50 55 60
 Glu Ile Ala Glu Ile His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly
 65 70 75 80
 Ala Pro Asn Glu Glu Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val
 85 90 95
 Glu Leu Pro Val Thr Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile
 100 105 110
 Ala Ile Ala Gln Gln Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala
 115 120 125
 Ala Ala Ala Cys Gln Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly
 130 135 140
 Ala Ile Leu Glu Arg Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met
 145 150 155 160
 Leu Phe Pro Ser Glu Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr
 165 170 175
 Arg Gln Arg Phe Met Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly
 180 185 190
 Ala His Ala Val Asn Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly
 195 200 205
 Trp Glu Ser Gly Trp Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val
 210 215 220

006290* 8026680

Asn Gly Ser Asn Pro Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr
 225 230 235 240
 Phe Gln Gly Gly Arg Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln
 245 250 255
 Val Ala Ser Ile Asn Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly
 260 265 270
 Gly Pro Asp Ser Asp Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr
 275 280 285
 Ala Asp Gly Val Gly Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr
 290 295 300
 Trp His Pro Gln His Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser
 305 310 315 320
 Ile Trp Arg Glu Glu Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile
 325 330 335
 Gly Asp Pro Glu Lys Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu
 340 345 350
 Lys Gly Glu Leu Ala Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe
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 Ile Glu Phe Leu Pro Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe
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 Glu Asn Gly Leu Ser Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala
 385 390 395 400
 Lys Lys Asp Ser Ile Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val
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 Arg Thr Lys Ser Asp Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe
 420 425 430
 Lys Ala Arg Met Asp Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val
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 Gly Tyr Gly Trp Ile Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala
 450 455 460
 Ala Tyr Ala Gln Gln Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr
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 Asn Leu Glu Ala Gly Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(433)

<223> RXN02949

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Asn	Ser	Gly	Val	Gly	Gly	Thr	Ser	Arg	Pro	Thr	Gly	Lys	Arg	Gln	Leu	
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tgc	ggt	gct	tcc	act	acc	tct	acc	tct	tct	tat	gag	gct	aag	cag	gta	211
Ser	Gly	Ala	Ser	Thr	Thr	Ser	Thr	Ser	Ser	Tyr	Glu	Ala	Lys	Gln	Val	
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tct	aca	cag	aag	aag	tca	tcc	ggt	tcg	gat	tct	aag	cct	ggc	ggc	ggt	259
Ser	Thr	Gln	Lys	Lys	Ser	Ser	Gly	Ser	Asp	Ser	Lys	Pro	Gly	Gly	Gly	
		40					45					50				

gtt	att	tct	ttt	ctg	cct	gag	gtt	gtg	gga	gaa	gtc	cgt	aag	gtt	att	307
Val	Ile	Ser	Phe	Leu	Pro	Glu	Val	Val	Gly	Glu	Val	Arg	Lys	Val	Ile	
	55					60					65					

tgg	cct	act	gcg	cgc	cag	atg	gtc	acg	tac	acc	ctt	gtc	gtt	ttg	gga	355
Trp	Pro	Thr	Ala	Arg	Gln	Met	Val	Thr	Tyr	Thr	Leu	Val	Val	Leu	Gly	
	70			75					80					85		

ttc	ttg	att	gtt	ttg	acc	gct	ttg	gtg	tct	ggt	gtg	gat	ttc	cta	gct	403
Phe	Leu	Ile	Val	Leu	Thr	Ala	Leu	Val	Ser	Gly	Val	Asp	Phe	Leu	Ala	
			90					95					100			

ggt	ctt	gga	gtt	gag	aag	att	ctg	act	ccg	taggtaggat	gtgtaacatc	453
Gly	Leu	Gly	Val	Glu	Lys	Ile	Leu	Thr	Pro			
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ttt												456
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<211> 111

<212> PRT

<213> Corynebacterium glutamicum

<400> 54

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Gly	Lys	Arg	Gln	Leu	Ser	Gly	Ala	Ser	Thr	Thr	Ser	Thr	Ser	Ser	Tyr
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Glu	Ala	Lys	Gln	Val	Ser	Thr	Gln	Lys	Lys	Ser	Ser	Gly	Ser	Asp	Ser
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Lys Pro Gly Gly Gly Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu
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 Val Arg Lys Val Ile Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr
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 <211> 1941
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1918)
 <223> RXN02462

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 Met Thr Lys Asp Val
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 cac tac gaa gtc gac gaa cgt aaa aag acc gtc ggt gtg aaa gaa gaa 163
 His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val Gly Val Lys Glu Glu
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 ggc gtc gaa tac gtc gaa gac caa ctc ggc atc gac aac ctc tac gca 211
 Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile Asp Asn Leu Tyr Ala
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 cct gag cac tca cag ctg gtc agc tac ctg aac aac gcc atc aag gca 259
 Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn Asn Ala Ile Lys Ala
 40 45 50
 cag gaa ctg ttc acc cgc gac aag gac tac atc gtc cgc aac ggc gaa 307
 Gln Glu Leu Phe Thr Arg Lys Asp Tyr Ile Val Arg Asn Gly Glu
 55 60 65
 gtt atg atc gtc gac ggc ttc acc ggc cgt gtc ctt gcc ggc cgc cga 355
 Val Met Ile Val Asp Gly Phe Thr Gly Arg Val Leu Ala Gly Arg Arg
 70 75 80 85
 tac aac gaa ggc atg cac cag gcg atc gaa gcc aaa gag cgc gta gag 403
 Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala Lys Glu Arg Val Glu
 90 95 100
 atc aaa aac gag aac cag acc ctg gcg acc gtt acc ctc cag aac tac 451
 Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val Thr Leu Gln Asn Tyr
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 Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr
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cca acc aac cga cca aac cag cgc gaa gac ttg acc gac ttg gtg tac 595
 Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu Thr Asp Leu Val Tyr
 150 155 160 165

aaa acc caa gag gct aag ttc gca gca gtc gtc gac gac atc gca gaa 643
 Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val Asp Asp Ile Ala Glu
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cgc acc gaa aag ggc caa cca gtc ctc gtc ggt acc gtc tcc gtc gag 691
 Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly Thr Val Ser Val Glu
 185 190 195

cgc tcc gaa tac ctc tcc cag ctg ttg acc aaa cga ggc atc aag cac 739
 Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys Arg Gly Ile Lys His
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aac gtc ctc aat gcg aag cac cac gag cag gaa gca cag atc gtt gct 787
 Asn Val Leu Asn Ala Lys His His Glu Gln Glu Ala Gln Ile Val Ala
 215 220 225

cag gca ggt ctt cca ggc gcc gtc acc gtt gcc acc aac atg gcg gcc 835
 Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala Thr Asn Met Ala Gly
 230 235 240 245

cgt gga acc gac atc gtg ctc ggc gga aac cca gaa atc ctc ctc gac 883
 Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro Glu Ile Leu Leu Asp
 250 255 260

atc aaa ctc cgc gaa cgt gga ctt gat cct ttc gaa gac gaa gaa agc 931
 Ile Lys Leu Arg Glu Arg Gly Leu Asp Pro Phe Glu Asp Glu Glu Ser
 265 270 275

tac cag gaa gcc tgg gac gct gaa ctt cca gca atg aag cag cga tgc 979
 Tyr Gln Glu Ala Trp Asp Ala Glu Leu Pro Ala Met Lys Gln Arg Cys
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gaa gaa cgt gcc gac aaa gtc cgc gaa gcc gga gga ctc tac gtc ctt 1027
 Glu Glu Arg Gly Asp Lys Val Arg Glu Ala Gly Gly Leu Tyr Val Leu
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cgt tct gca cgt cag gcc gac cca gga tcc acc cgc ttc tat ctc tct 1123
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 345 350 355

atg atg aac agg ctc aac gtc cca gac gat gtg ccc atc gaa tcc aaa 1219
 Met Met Asn Arg Leu Asn Val Pro Asp Asp Val Pro Ile Glu Ser Lys
 360 365 370

002290-80229060

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 Thr Val Thr Asn Ser Ile Lys Gly Ala Gln Ala Gln Val Glu Asn Gln
 375 380 385

aac ttc gaa atg cgt aag aac gtt ctg aag tac gac gaa gtc atg aac 1315
 Asn Phe Glu Met Arg Lys Asn Val Leu Lys Tyr Asp Glu Val Met Asn
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gaa cag cgc aag gtt atc tac agc gag cga cgc gaa atc ctc gaa tcc 1363
 Glu Gln Arg Lys Val Ile Tyr Ser Glu Arg Glu Ile Leu Glu Ser
 410 415 420

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 Ala Asp Ile Ser Arg Tyr Ile Gln Asn Met Ile Glu Glu Thr Val Ser
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 Ala Tyr Val Asp Gly Ala Thr Ala Asn Gly Tyr Val Glu Asp Trp Asp
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ctc gac aaa ctc tgg aac gcc ctc gaa gcc ctc tac gac cca tcg atc 1507
 Leu Asp Lys Leu Trp Asn Ala Leu Glu Ala Leu Tyr Asp Pro Ser Ile
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 Asn Trp Thr Asp Leu Val Glu Gly Ser Glu Tyr Gly Lys Pro Gly Glu
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ctg tcc gcc gaa gat cta cgc acc gca ctc gtc aac gac gcc cac gcc 1603
 Leu Ser Ala Glu Asp Leu Arg Thr Ala Leu Val Asn Asp Ala His Ala
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cag atc cgc aac atc gaa cga atg gtg ctc atg cca gtc atc gac acc 1699
 Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met Pro Val Ile Asp Thr
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 Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr Leu Lys Glu Gly Ile
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 Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu Val Glu Tyr Gln Lys
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gaa ggc ggc gac atg ttc aac ggc atg aaa gac ggc atc aag gaa gaa 1843
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 570 575 580

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 Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser Ser Ser Ser Lys Thr
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<213> *Corynebacterium glutamicum*

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Asn Ala Ile Lys Ala Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile
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Val Arg Asn Gly Glu Val Met Ile Val Asp Gly Phe Thr Gly Arg Val
 65 70 75 80

Leu Ala Gly Arg Arg Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala
 85 90 95

Lys Glu Arg Val Glu Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val
 100 105 110

Thr Leu Gln Asn Tyr Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr
 115 120 125

Gly Thr Ala Glu Thr Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu
 130 135 140

Asp Val Ile Ala Ile Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu
 145 150 155 160

Thr Asp Leu Val Tyr Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val
 165 170 175

Asp Asp Ile Ala Glu Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly
 180 185 190

Thr Val Ser Val Glu Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys
 195 200 205

Arg Gly Ile Lys His Asn Val Leu Asn Ala Lys His His Glu Gln Glu
 210 215 220

Ala Gln Ile Val Ala Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala
 225 230 235 240

Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro
 245 250 255

Glu Ile Leu Leu Asp Ile Lys Leu Arg Glu Arg Gly Leu Asp Pro Phe
 260 265 270

Glu Asp Glu Glu Ser Tyr Gln Glu Ala Trp Asp Ala Glu Leu Pro Ala
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Met Lys Gln Arg Cys Glu Glu Arg Gly Asp Lys Val Arg Glu Ala Gly
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 Gly Leu Tyr Val Leu Gly Thr Glu Arg His Glu Ser Arg Arg Ile Asp
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 Asn Gln Leu Arg Gly Arg Ser Ala Arg Gln Gly Asp Pro Gly Ser Thr
 325 330 335
 Arg Phe Tyr Leu Ser Met Arg Asp Asp Leu Met Val Arg Phe Val Gly
 340 345 350
 Pro Thr Met Glu Asn Met Met Asn Arg Leu Asn Val Pro Asp Asp Val
 355 360 365
 Pro Ile Glu Ser Lys Thr Val Thr Asn Ser Ile Lys Gly Ala Gln Ala
 370 375 380
 Gln Val Glu Asn Gln Asn Phe Glu Met Arg Lys Asn Val Leu Lys Tyr
 385 390 395 400
 Asp Glu Val Met Asn Glu Gln Arg Lys Val Ile Tyr Ser Glu Arg Arg
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 Glu Glu Thr Val Ser Ala Tyr Val Asp Gly Ala Thr Ala Asn Gly Tyr
 435 440 445
 Val Glu Asp Trp Asp Leu Asp Lys Leu Trp Asn Ala Leu Glu Ala Leu
 450 455 460
 Tyr Asp Pro Ser Ile Asn Trp Thr Asp Leu Val Glu Gly Ser Glu Tyr
 465 470 475 480
 Gly Lys Pro Gly Glu Leu Ser Ala Glu Asp Leu Arg Thr Ala Leu Val
 485 490 495
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 Pro Val Ile Asp Thr Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr
 530 535 540
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 Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp
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<223> RXN01559
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				Val	Leu	Ile	Val	Val												
				1				5												
gggt gtt tat	gcg ttg	ctg ttg	aca ggc	gat cgt	tct gcc	aca cca	163													
Gly Val Tyr	Ala Leu	Val Leu	Leu Thr	Gly Asp	Arg Ser	Ala Thr														
		10		15		20														
aaa ttg ggt att	gat ctg	caa ggc	gga acc	cga gtg	acc ctc	gtg ccg	211													
Lys Leu Gly	Ile Asp	Leu Gln	Gly Gly	Thr Arg	Val Thr	Leu Val														
		25		30		35														
cag ggg cag gat	cca act	cag gac	cag ctg	aat cag	gca cgc	acc att	259													
Gln Gly Gln	Asp Pro	Gln Asp	Gln Leu	Asn Gln	Ala Arg	Thr Ile														
		40		45		50														
ctg gaa aac cgt	gtg aac	ggc atg	ggc gtt	tca ggt	gca agc	gtg gtc	307													
Leu Glu Asn	Arg Val	Asn Gly	Met Gly	Val Ser	Gly Ala	Ser Val														
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gct gac ggt aac	acg ctg	gtg atc	act gtt	ccc ggg	gaa aat	acc gca	355													
Ala Asp Gly	Asn Thr	Leu Val	Ile Thr	Val Pro	Gly Glu	Asn Thr														
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cag gcg caa tcc	cta gga	cag acc	tcc cag	ctg ctg	ttc cgt	ccc gtt	403													
Gln Ala Gln	Ser Leu	Gly Gln	Thr Ser	Gln Leu	Leu Phe	Arg Pro														
		90		95		100														
gggt cag gca gga	atg ccc	gat acc	acg ttg	atg cca	gag gtc	gtg gaa	451													
Gly Gln Ala	Gly Met	Pro Asp	Met Thr	Thr Leu	Met Pro	Glu Leu														
		105		110		115														
gag atg gcc aac	agg tgg	ggt gaa	tac ggc	gtc atc	acc gaa	gag cag	499													
Glu Met Ala	Asn Arg	Trp Val	Glu Tyr	Gly Val	Ile Thr	Glu Thr														
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gca aat gcc tcc	ttg gag	gaa atg	aac acc	gct gtt	gca tcg	acc act	547													

096031131015300

cgc cag gaa atc acg gac atg ctg cgc acc gac cgc cag tcc acc gat 691
 Arg Gln Glu Ile Thr Asp Met Leu Arg Thr Asp Arg Gln Ser Thr Asp
 185 190 195

ccc act gtc cag atc gct gca agt tct ttg atg cag tgc acc act gat 739
 Pro Thr Val Gln Ile Ala Ala Ser Ser Leu Met Gln Cys Thr Thr Asp
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gag atg gat cct ttg gcc ggc acc gat gat cca cgc ctg cca ttg gtg 787
 Glu Met Asp Pro Leu Ala Gly Thr Asp Asp Pro Arg Leu Pro Leu Val
 215 220 225

gca tgt gat cca gct gta ggt ggc gtg tat gta ctt gat cct gca cct 835
 Ala Cys Asp Pro Ala Val Gly Gly Val Tyr Val Leu Asp Pro Ala Pro
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aat gag atc gat acc aac cgt ccc atc acc ggt gga ttc aac gcc cag 931
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 Gln Ile Ala Ile Thr Leu Asp Ser Gln Val Ile Ser Ala Pro Val Ile
 310 315 320 325

cag tca gca acc cct gtg ggt tct gca aca tcc atc acc ggt gac ttc 1123
 Gln Ser Ala Thr Pro Val Gly Ser Ala Thr Ser Ile Thr Gly Asp Phe
 330 335 340

act caa act gaa gcc caa gat ctg gcg aac aac ctg cgc tac ggt gca 1171
 Thr Gln Thr Glu Ala Gln Asp Leu Ala Asn Asn Leu Arg Tyr Gly Ala
 345 350 355

ttg ccc ctg agc ttc gca ggt gaa aac ggc gag cgc ggc gga act acc 1219
 Leu Pro Leu Ser Phe Ala Gly Glu Asn Gly Glu Arg Gly Gly Thr Thr
 360 365 370

acc acc gtt ccg cca tca cta ggc gca gca tcc ttg aag gcc gga ctg 1267
 Thr Thr Val Pro Pro Ser Leu Gly Ala Ala Ser Leu Lys Ala Gly Leu
 375 380 385

atc gca ggc atc gtc ggc atc gcg ctg gtc gcc atc ttc gtg ttc gcc 1315
 Ile Ala Gly Ile Val Gly Ile Ala Leu Val Ala Ile Phe Val Phe Ala
 390 395 400 405

tac tac cgc gtc ttc gga ttc gtt tcc ctg ttc acc ctg ttt gcc gca 1363
 Tyr Tyr Arg Val Phe Gly Phe Val Ser Leu Phe Thr Leu Phe Ala Ala
 410 415 420

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 Gly Val Leu Val Tyr Gly Leu Leu Val Leu Leu Gly Arg Trp Ile Gly
 425 430 435

tat tcc cta gac ctt gct ggt atc gcc ggt ttg atc atc ggt atc ggt 1459
 Tyr Ser Leu Asp Leu Ala Gly Ile Ala Gly Leu Ile Ile Gly Ile Gly
 440 445 450

acc acc gcc gac tcc ttc gtg gtg ttc tat gag cgc atc aag gat gag 1507
 Thr Thr Ala Asp Ser Phe Val Val Phe Tyr Glu Arg Ile Lys Asp Glu
 455 460 465

atc cgt gaa gga aga tcc ttt aga tct gca gta cct cgt gca tgg gaa 1555
 Ile Arg Glu Gly Arg Ser Phe Arg Ser Ala Val Pro Arg Ala Trp Glu
 470 475 480 485

agc gcc aag cgc acc atc gtc aca ggc aac atg gtc act ttg ctc ggc 1603
 Ser Ala Lys Arg Thr Ile Val Thr Gly Asn Met Val Thr Leu Leu Gly
 490 495 500

gct atc gtg att tac ttg ctc gcg gtc gcc gaa gtc aag gcc ttt gcc 1651
 Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu Val Lys Gly Phe Ala
 505 510 515

ttc acc ctg ggt ctg acc acc gta ttc gat ctc gtt gtc acc ttc ctg 1699
 Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu Val Val Thr Phe Leu
 520 525 530

atc acg gca cca ctg gtt atc ctg gca tca cgc aac cca ttc ttt gcc 1747
 Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg Asn Pro Phe Phe Ala
 535 540 545

aag tca tcg gtc aac ggc atg gga cga gtg atg aag ctc gtt gaa gaa 1795
 Lys Ser Ser Val Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu
 550 555 560 565

cgc cgc gcc aac ggt gaa ttg gat gag cct gag tac ctg aaa aag atc 1843
 Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile
 570 575 580

cat gcc aag aat gcg gca gct gat aag gct tcc act gac aat tct tcc 1891
 His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser
 585 590 595

act gac aat tct gaa gca cct gcc acc gat acg aac caa gag gag gag 1939
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<210> 58

<211> 614

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

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006290-802690

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 Val Thr Leu Val Pro Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu Asn
 35 40 45
 Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val Ser
 50 55 60
 Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val Pro
 65 70 75 80
 Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln Leu
 85 90 95
 Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr Leu
 100 105 110
 Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly Val
 115 120 125
 Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr Ala
 130 135 140
 Val Ala Ser Thr Thr Ala Val Glu Gly Glu Glu Ala Thr Glu Pro Glu
 145 150 155 160
 Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser Ile
 165 170 175
 Glu Ala Thr Gln Arg Arg Gln Glu Ile Thr Asp Met Leu Arg Thr Asp
 180 185 190
 Arg Gln Ser Thr Asp Pro Thr Val Gln Ile Ala Ala Ser Ser Leu Met
 195 200 205
 Gln Cys Thr Thr Asp Glu Met Asp Pro Leu Ala Gly Thr Asp Asp Pro
 210 215 220
 Arg Leu Pro Leu Val Ala Cys Asp Pro Ala Val Gly Gly Val Tyr Val
 225 230 235 240
 Leu Asp Pro Ala Pro Leu Leu Asn Gly Glu Thr Asp Glu Glu Asn Gly
 245 250 255
 Ala Arg Leu Thr Gly Asn Glu Ile Asp Thr Asn Arg Pro Ile Thr Gly
 260 265 270
 Gly Phe Asn Ala Gln Ser Gly Gln Met Glu Ile Ser Phe Ala Phe Lys
 275 280 285
 Ser Gly Asp Gly Glu Glu Gly Ser Ala Thr Trp Ser Ser Leu Thr Ser
 290 295 300
 Gln Tyr Leu Gln Gln Gln Ile Ala Ile Thr Leu Asp Ser Gln Val Ile
 305 310 315 320
 Ser Ala Pro Val Ile Gln Ser Ala Thr Pro Val Gly Ser Ala Thr Ser
 325 330 335

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Ile Thr Gly Asp Phe Thr Gln Thr Glu Ala Gln Asp Leu Ala Asn Asn
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 Leu Arg Tyr Gly Ala Leu Pro Leu Ser Phe Ala Gly Glu Asn Gly Glu
 355 360 365
 Arg Gly Gly Thr Thr Thr Thr Val Pro Pro Ser Leu Gly Ala Ala Ser
 370 375 380
 Leu Lys Ala Gly Leu Ile Ala Gly Ile Val Gly Ile Ala Leu Val Ala
 385 390 395 400
 Ile Phe Val Phe Ala Tyr Tyr Arg Val Phe Gly Phe Val Ser Leu Phe
 405 410 415
 Thr Leu Phe Ala Ala Gly Val Leu Val Tyr Gly Leu Leu Val Leu Leu
 420 425 430
 Gly Arg Trp Ile Gly Tyr Ser Leu Asp Leu Ala Gly Ile Ala Gly Leu
 435 440 445
 Ile Ile Gly Ile Gly Thr Thr Ala Asp Ser Phe Val Val Phe Tyr Glu
 450 455 460
 Arg Ile Lys Asp Glu Ile Arg Glu Gly Arg Ser Phe Arg Ser Ala Val
 465 470 475 480
 Pro Arg Ala Trp Glu Ser Ala Lys Arg Thr Ile Val Thr Gly Asn Met
 485 490 495
 Val Thr Leu Leu Gly Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu
 500 505 510
 Val Lys Gly Phe Ala Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu
 515 520 525
 Val Val Thr Phe Leu Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg
 530 535 540
 Asn Pro Phe Phe Ala Lys Ser Ser Val Asn Gly Met Gly Arg Val Met
 545 550 555 560
 Lys Leu Val Glu Glu Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu
 565 570 575
 Tyr Leu Lys Lys Ile His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser
 580 585 590
 Thr Asp Asn Ser Ser Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr
 595 600 605
 Asn Gln Glu Glu Glu Lys
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<211> 819

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(796)

<223> RXN00046

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 Met Asp Leu Asn Thr
 1 5

caa cgc tca aag ctc tac gca cag ctt caa ggc cag ctc att gtt tcc 163
 Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly Gln Leu Ile Val Ser
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gtg caa gct ccc gac ggc cat gcc atg cga gat acc cat acg ctc acc 211
 Val Gln Ala Pro Asp Gly His Ala Met Arg Asp Thr His Thr Leu Thr
 25 30 35

cat gtg gcc gca gcc tgt gtc gat ggc ggt gct cct gcc att cgc tgt 259
 His Val Ala Ala Cys Val Asp Gly Gly Ala Pro Ala Ile Arg Cys
 40 45 50

ggc ggt tac ggc ggt ttg gaa gat atc cgt tca atc tcc aac cgt gtc 307
 Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser Ile Ser Asn Arg Val
 55 60 65

gac gtt ccc gtt ttc gga ctc acc aaa gaa ggc tcc gaa gga gtt tac 355
 Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly Ser Glu Gly Val Tyr
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atc acc cca acc agg gat tcc gtt cga gca gtg gca gaa tcc ggc gcc 403
 Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val Ala Glu Ser Gly Ala
 90 95 100

act gta gtc tgc gcg gat gca act ttc cga cct agg cct gac ggc tcc 451
 Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro Arg Pro Asp Gly Ser
 105 110 115

acc ttt gca gag ctg gtc act gtt gcc cac gat tcc gga att ctc atc 499
 Thr Phe Ala Glu Leu Val Thr Val Ala His Asp Ser Gly Ile Leu Ile
 120 125 130

atg gcg gac tgc gca act ccc gaa gaa gtt ctc agt gcg cat aag gct 547
 Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu Ser Ala His Lys Ala
 135 140 145

ggc gcg gat ttt gtg tcc acc acg ett gct gga tac acc gaa cac cgc 595
 Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly Tyr Thr Glu His Arg
 150 155 160 165

gag aaa aca gtc ggt cca gat ttc gat tgc ctc cgc gaa gca cgt gag 643
 Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu Arg Glu Ala Arg Glu
 170 175 180

tta gtt ccc gat gcg ttc ctc att ggc gaa ggt cgc ttc tcc aac cct 691
 Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly Arg Phe Ser Asn Pro
 185 190 195

gcg gat gtg gcg cac ggt cgt ctc att ggt gcc aac gcg atc atc gtg 739
 Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala Asn Ala Ile Ile Val

006290.802E0960

200 205 210
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 ctg ttg cac tagcacttag tccagcgctg cac 819
 Leu Leu His
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 Gln Leu Ile Val Ser Val Gln Ala Pro Asp Gly His Ala Met Arg Asp
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 Thr His Thr Leu Thr His Val Ala Ala Ala Cys Val Asp Gly Gly Ala
 35 40 45
 Pro Ala Ile Arg Cys Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser
 50 55 60
 Ile Ser Asn Arg Val Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly
 65 70 75 80
 Ser Glu Gly Val Tyr Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val
 85 90 95
 Ala Glu Ser Gly Ala Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro
 100 105 110
 Arg Pro Asp Gly Ser Thr Phe Ala Glu Leu Val Thr Val Ala His Asp
 115 120 125
 Ser Gly Ile Leu Ile Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu
 130 135 140
 Ser Ala His Lys Ala Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly
 145 150 155 160
 Tyr Thr Glu His Arg Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu
 165 170 175
 Arg Glu Ala Arg Glu Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly
 180 185 190
 Arg Phe Ser Asn Pro Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala
 195 200 205
 Asn Ala Ile Ile Val Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr
 210 215 220
 Gly Gln Phe Ala Ser Leu Leu His
 225 230

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Val Lys Leu Lys Gln Pro Val Ser Ile Tyr Asn Asp Pro Trp Glu Ser																			
																		5 10 15	
tat aac gat gtt aaa gaa cat gcc caa tta act tta agt aac atc gaa	152																		
Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser Asn Ile Glu																			
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ttt acs act acs aat ctt tgt aat atg cgt tgt agc cac tgt gcs gtt	200																		
Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His Cys Ala Val																			
																		40 45 50	
gggt tat act tta caa act gtc gac ccc gag cct tta gat atg gac tta	248																		
Gly Tyr Thr Thr Leu Gln Thr Val Asp Pro Glu Pro Leu Asp Met Asp Leu																			
																		55 60 65	
att tat cgt aga ctt gat gaa att cca aat ctg cga acg atg tca att	296																		
Ile Tyr Arg Arg Leu Asp Glu Ile Pro Asn Leu Arg Thr Met Ser Ile																			
																		70 75 80	
aca ggt gcc gaa cca atg ttt tct aaa aag tct att aga aat gtt gtt	344																		
Thr Gly Gly Glu Pro Met Phe Ser Lys Lys Ser Ile Arg Asn Val Val																			
																		85 90 95	
aaa cct cta tta aag tat gca cat cat cga ggt ata tat aca caa atg	392																		
Lys Pro Leu Leu Lys Tyr Ala His His Arg Gly Ile Tyr Thr Gln Met																			
																		100 105 110 115	
aat tca aac cta acc ttg cct caa gat cgt tat tta gat att gct gaa	440																		
Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp Ile Ala Glu																			
																		120 125 130	
tat atc gat gtt atg cat atc tca cat aac tgg gga acc act gat gaa	488																		
Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr Asp Glu																			
																		135 140 145	
ttc gca aat gtt gcc ttt gcc gca atg aag aag caa cca ccg tta aaa	536																		
Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro Pro Leu Lys																			
																		150 155 160	
gct aag tta aaa tta tat gaa caa atg att tcg aat gca cgt acc tta	584																		
Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala Arg Thr Leu																			
																		165 170 175	

056303-0620

tca gaa caa gga atg ttt gta tct gcg gaa aca atg ctc aat caa agt 632
 Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu Asn Gln Ser 195
 180 185 190

acg cta cca cat tta cga aaa ata cat caa gaa gtc gtt cat gat atg 680
 Thr Leu Pro His Leu Arg Lys Ile His Gln Val Val His Asp Met 210
 200 205

aaa tgt agc aga cac gag att cac cct atg tat cca gct gac ttt gca 728
 Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala Asp Phe Ala 225
 215 220

agt caa tta aat gtg tta act cta gcg gaa atg aaa aag aca att cat 776
 Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys Thr Ile His 240
 230 235

gat ata ttg gat ttc aga gat gaa gat att tgg atg tta ttt ggt act 824
 Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu Phe Gly Thr 255
 245 250

ttg cct gtg ttt cca tgc tta aag gat gat gaa gat caa aag tta cta 872
 Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln Lys Leu Leu 275
 260 265

tca cgt tta aga aat gct aac aat gta acg act aga aat gac ccg gat 920
 Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn Asp Pro Asp 290
 280 285

ggc cgt agt cgt tta aat gtc aat gta ttt aca ggt aat gta atc gta 968
 Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn Val Ile Val 305
 295 300

act gat ttc gga gat gaa aca ggt aca att tcg aat ata caa aaa gat 1016
 Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile Gln Lys Asp 320
 310 315

aaa tta aca gat gta ttt gat aaa tgg tta tcc tct gat ctt gct aaa 1064
 Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp Leu Ala Lys 335
 325 330

tca tta aat tgt cat tgt tcc gag ttt agt tgt tta gga cca aat gtt 1112
 Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly Pro Asn Val 355
 340 345

ctt gtt aaa aat atg tac tat ccg aat atg gat ttt aaa gat aat gag 1160
 Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys Asp Asn Glu 370
 360 365

cgt cat atg cac aaa caa cca caa att ata caa ttt taaaaactct 1206
 Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe 380
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taattatgcg gag 1219

<210> 62

<211> 383

<212> PRT

<213> Corynebacterium glutamicum

<400> 62

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 Trp Glu Ser Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser
 20 25 30
 Asn Ile Glu Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His
 35 40 45
 Cys Ala Val Gly Tyr Thr Leu Gln Thr Val Asp Pro Glu Pro Leu Asp
 50 55 60
 Met Asp Leu Ile Tyr Arg Arg Leu Asp Glu Ile Pro Asn Leu Arg Thr
 65 70 75 80
 Met Ser Ile Thr Gly Gly Glu Pro Met Phe Ser Lys Lys Ser Ile Arg
 85 90 95
 Asn Val Val Lys Pro Leu Leu Lys Tyr Ala His His Arg Gly Ile Tyr
 100 105 110
 Thr Gln Met Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp
 115 120 125
 Ile Ala Glu Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr
 130 135 140
 Thr Asp Glu Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro
 145 150 155 160
 Pro Leu Lys Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala
 165 170 175
 Arg Thr Leu Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu
 180 185 190
 Asn Gln Ser Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val
 195 200 205
 His Asp Met Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala
 210 215 220
 Asp Phe Ala Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys
 225 230 235 240
 Thr Ile His Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu
 245 250 255
 Phe Gly Thr Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln
 260 265 270
 Lys Leu Leu Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn
 275 280 285
 Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn
 290 295 300
 Val Ile Val Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile
 305 310 315 320
 Gln Lys Asp Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp

00603200-062300

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atc gtc gtc gat gaa aac ggc aag gtt gct tac acc cag ttg gtt gat 547
 ile val val asp glu asn gly lys val ala tyr thr gln leu val asp
 135 140 145

gag atc ttc act gaa cct gat tac gac gct gca ctt gct ggg ctg aac 595
 glu ile phe thr glu pro asp tyr asp ala ala leu ala gly leu asn
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taatttactt cgctcagggg aat 618

<210> 64

<211> 165

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 64

Met Ala Lys Thr His Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu
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Leu Pro Gln Val Gly Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr
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Glu Leu Gly Glu Val Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val
 35 40 45

Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val
 50 55 60

Arg Lys Phe Asn Glu Ala Ala Ser Leu Glu Asn Thr Thr Val Leu
 65 70 75 80

Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala
 85 90 95

Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe
 100 105 110

Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu
 115 120 125

Leu Ala Arg Ser Val Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr
 130 135 140

Thr Gln Leu Val Asp Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala
 145 150 155 160

Leu Ala Gly Leu Asn
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<210> 65

<211> 879

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(856)

<223> RXN01676

002290-80229600

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accagcattt ttgtcatcct cagtggggtgc tggcccgcg atg atc ctt cac ggt 115
Met Ile Leu His Gly
1 5

ggt gtg ttc tac gca gga ctt cta gta ctt ctc gtg cca ctt ggc ctt 163
Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu Val Pro Leu Gly Leu
10 15 20

ggt gcg gga atc ctc gcc gag ctg ttt atc acc caa cgc cag acc atc 211
Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr Gln Arg Gln Thr Ile
25 30 35

atc gtg gtt tca tog atc gtg ctg att atc cta ggt ttt gtc cag atc 259
Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu Gly Phe Val Gln Ile
40 45 50

ttc gcc gcc gga ttc gac ttc gga aaa gca ctc cca gga tta gat cgt 307
Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu Pro Gly Leu Asp Arg
55 60 65

ctg caa tct aag gcc act gtg acc tca ggt cta gga aag agc ttt tta 355
Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu Gly Lys Ser Phe Leu
70 75 80 85

cta gga atg acc agt agt att gcc ggt ttt tgt tcc gga cca atc ctc 403
Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys Ser Gly Pro Ile Leu
90 95 100

ggc gcc gtt ctt act ttg gct gcc acc agt gga aac tcc atc acc tca 451
Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly Asn Ser Ile Thr Ser
105 110 115

gca ctc att ttg agt gct tat ggt gcg gga atg gtg ctg ccc ctg atg 499
Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met Val Leu Pro Leu Met
120 125 130

gct att gca gcg ctc tgg gcc aaa ctc gga cag cgt gga cag cag atg 547
Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln Arg Gly Gln Gln Met
135 140 145

ctc cgc gcc cgg gaa ttc acc ttc ttg gcc agg cag tgg cac att gtt 595
Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg Gln Trp His Ile Val
150 155 160 165

tct gtc att agc ggt gcc ctg atc atc gct gtc gga atc ctc ttt tgg 643
Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val Gly Ile Leu Phe Trp
170 175 180

tcc aog aac gcc ctt gtc agc atg ccg gag ctc gtt cca atg gac acc 691
Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu Val Pro Met Asp Thr
185 190 195

cag atc tgg cta cag gaa gcc aca ttc tca ctc ggg tca cca ctc ttt 739
Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu Gly Ser Pro Leu Phe
200 205 210

gac atc gca ttg atc att gtc gcc gct gcc ttg ttc ttg tac ttc tgg 787
Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu Phe Leu Tyr Phe Trp

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215 220 225
 aac aaa cga caa aag cga aaa gaa gaa gct cag cga ccc aaa gaa agt 835
 Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln Arg Pro Lys Glu Ser
 230 235 240 245

 gga tgg gtt att aac cct cgc taattattag ttttggagcg agg 879
 Gly Trp Val Ile Asn Pro Arg
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 <210> 66
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 <213> Corynebacterium glutamicum

 <400> 66
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 Gln Arg Gln Thr Ile Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu
 35 40 45

 Gly Phe Val Gln Ile Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu
 50 55 60

 Pro Gly Leu Asp Arg Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu
 65 70 75 80

 Gly Lys Ser Phe Leu Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys
 85 90 95

 Ser Gly Pro Ile Leu Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly
 100 105 110

 Asn Ser Ile Thr Ser Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met
 115 120 125

 Val Leu Pro Leu Met Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln
 130 135 140

 Arg Gly Gln Gln Met Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg
 145 150 155 160

 Gln Trp His Ile Val Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val
 165 170 175

 Gly Ile Leu Phe Trp Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu
 180 185 190

 Val Pro Met Asp Thr Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu
 195 200 205

 Gly Ser Pro Leu Phe Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu
 210 215 220

 Phe Leu Tyr Phe Trp Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln
 225 230 235 240

00603208.062300

Arg Pro Lys Glu Ser Gly Trp Val Ile Asn Pro Arg
245 250

<210> 67
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<212> DNA
<213> *Corynebacterium glutamicum*

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<222> (101)..(721)
<223> RXN00380

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Val Arg Leu Thr Lys
1 5
cta gca gca aca atc ggc tgc gtg aca ctc agc gga ctt gcg cta gta 163
Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser Gly Leu Ala Leu Val
10 15 20
gcc tgc agc agt gac agt acc gct ggt act gac gct gtt gct gtc ggc 211
Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp Ala Val Ala Val Gly
25 30 35
gga acc ttc caa ttc cac tcc ccg gat gga aag atg gaa att ttc tac 259
Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys Met Glu Ile Phe Tyr
40 45 50
gac gag gct gac cgt caa caa ctc ccc gac att ggt gga gat tcc ctc 307
Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile Gly Gly Asp Ser Leu
55 60 65
atg gaa gag ggc aca cag atc aac ctg tct gat ttc gaa aac caa gtt 355
Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp Phe Glu Asn Gln Val
70 75 80 85
gtc atc ctc aat gcg tgg ggg cag tgg tgt gca ccg tgc cgc tcc gaa 403
Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala Pro Cys Arg Ser Glu
90 95 100
tcc gat gat ctc cag att atc cat gag gaa ctc caa gct gcc gga aac 451
Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu Gln Ala Ala Gly Asn
105 110 115
ggc gac acc cct ggt ggc acc gtg ttg ggt atc aat gtg cgt gat tac 499
Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile Asn Val Arg Asp Tyr
120 125 130
tcc cgc gac atc gcc caa gac ttt gtc acc gac aac ggc ctt gat tac 547
Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp Asn Gly Leu Asp Tyr
135 140 145
cca agc att tac gat cca cca ttt atg aca gca gca tcc ctc ggt ggt 595
Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala Ala Ser Leu Gly Gly
150 155 160 165

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gtt ccc gca tcg gtg atc cca acc acc atc gtg ctg gat aaa cag cac 643
 Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val Leu Asp Lys Gln His
 170 175 180

cgc ccc gca gca gtg ttc ttg cgc gaa gtc acc tcc aaa gat gtg ttg 691
 Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr Ser Lys Asp Val Leu
 185 190 195

gat gtt cgc ttg cca ttg gta gat gag gcc taaatgtctg agattgtggt 741
 Asp Val Ala Leu Pro Leu Val Asp Glu Ala
 200 205

agc 744

<210> 68
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 <212> PRT
 <213> *Corynebacterium glutamicum*

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Gly Leu Ala Leu Val Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp
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Ala Val Ala Val Gly Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys
 35 40 45

Met Glu Ile Phe Tyr Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile
 50 55 60

Gly Gly Asp Ser Leu Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp
 65 70 75 80

Phe Glu Asn Gln Val Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala
 85 90 95

Pro Cys Arg Ser Glu Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu
 100 105 110

Gln Ala Ala Gly Asn Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile
 115 120 125

Asn Val Arg Asp Tyr Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp
 130 135 140

Asn Gly Leu Asp Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala
 145 150 155 160

Ala Ser Leu Gly Gly Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val
 165 170 175

Leu Asp Lys Gln His Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr
 180 185 190

Ser Lys Asp Val Leu Asp Val Ala Leu Pro Leu Val Asp Glu Ala
 195 200 205

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<400> 70
Met Ala Thr Ile Asp Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr
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Gly Asp Gly Ile Val Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro

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35	40	45
Asp Ala Thr Phe Ala Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala		
50	55	60
Ala Ala Leu Gln Ile Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp		
65	70	75
Gly Ile Met Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu		
85	90	95
Asp Asp Leu Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg		
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Arg Gln Val Ala Glu Gln Gln Gly Ser Ala Glu Ala		
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 Met Asp His Ala His
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 gat tcc tgc tca cca act ctg cgc cgt gat ttg gag gtc act ggc cag 163
 Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp Leu Glu Val Thr Gly Gln
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 ctc caa cct gag aaa gct gtc gat tta gca gcg ccg cac gaa ggg aag 211
 Leu Gln Pro Thr Lys Ala Val Asp Leu Ala Ala Pro His Glu Gly Lys
 25 30 35
 gtt gcc aat ata acg aag gtg acc tcc tca aat atg gag cac acc atc 259
 Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn Met Glu His Thr Ile
 40 45 50
 acg cag gcc tca aaa gct aag gag gtg gtg gtg ctc att ggt cac tcc 307
 Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val Leu Ile Gly His Ser
 55 60 65
 ctg ctg ccc aca ttt cag gat ttg gaa aaa gac att ctg cac ttt cag 355
 Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp Ile Leu His Phe Gln
 70 75 80 85
 gca ggt aat aaa ggg cga ttt tct gta gcg att gtt gat cct gat cgc 403
 Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile Val Asp Pro Asp Arg
 90 95 100

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 Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys Gln Ile Pro Val Ala
 105 110 115
 tac gtg gtg aaa gat ggc gcc agc att gcg gag ttc aac tcg ctc aac 499
 Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu Phe Val Ser Leu Asn
 120 125 130
 aag gag ccg gtt gca caa tgg ctt gat cat ttt gtg tcg cgg gaa acg 547
 Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe Val Ser Arg Glu Thr
 135 140 145
 atc ccc aat gaa aaa gag ggg gac gtc gat aag caa ata gac ccg cgc 595
 Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys Gln Ile Asp Pro Arg
 150 155 160
 ctg tgg ccg gca gcg gaa ttg gtg aac gcc ggt gat ttt cgc gcg gcg 643
 Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly Asp Phe Arg Ala Ala
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 ttg gcg ttg tat gag cag ttg ccg cag gat gcg acg gtg aag ccg gcg 691
 Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala Thr Val Lys Arg Ala
 185 190 195
 cac gcg gcg gtg tgc gta ttg gcg ccg atg tct gtg gcg gat ccg gga 739
 His Ala Ala Val Ser Val Leu Ala Arg Met Ser Val Ala Asp Arg Gly
 200 205 210
 gag gat ccg atc gag aag tcg cgc ccg gat cca gac gat gtg aac aag 787
 Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro Asp Val Asn Lys
 215 220 225
 gcg ctg gcg gcg gcg gat atg tat gtg ttg atg aat cag ccg gac aca 835
 Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met Asn Gln Pro Asp Thr
 230 235 240 245
 gcg ctc gcg cac ctt gca gca cta ttg cca aaa ccg gag gct gcc ccg 883
 Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys Pro Glu Ala Ala Arg
 250 255 260
 ccg atc gtg gag ttg ctg aac ttg ttt gat ccg ctg gac ctg gtc gca 931
 Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro Leu Asp Leu Val Ala
 265 270 275
 ttg gaa atc agg gcg cag gtg ggg aat gca atg agc taagaaaaa 977
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<211> 289

<212> PRT

<213> Corynebacterium glutamicum

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	Val	Ser	Thr	Asn	Lys	
		1			5	

gaa cga cgc caa cag gcg ctt tcc cag ctg gag aaa gaa atc aaa agc	163
Glu Arg Arg Gln Gln Ala Leu Ser Gln Leu Glu Lys Glu Ile Lys Ser	
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cgg gac cgc aaa gaa aag acc aag cca cta acc gtg gtc ttt gct tcc	211
Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr Val Val Phe Ala Ser	
	25 30 35

ctg gct gtc atc ctg gtt gtc gtt ggc ggt atc tgg tac gca gct acc	259
Leu Ala Val Ile Leu Val Val Val Gly Gly Ile Trp Tyr Ala Ala Thr	
	40 45 50

cgc agc acc gaa gac gaa gtc atc acc gct gat gaa aca tcc acc acc	307
Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp Glu Thr Ser Thr Thr	
	55 60 65

gca gag acc cct gac tac cag cca ctg gcg ctg acc cgc acc acc gcg	355
Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu Thr Arg Thr Thr Ala	
	70 75 80 85

ctc ggc gac tcc gtg acc tgt gag tac cca gat gct ggc gag gct tcc	403
Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp Ala Gly Glu Ala Ser	
	90 95 100

aag gat gtc tcc aag cct gct act gaa aac gtg cca gca acc ggc acc	451
Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val Pro Ala Thr Gly Thr	
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gtg acc gtc aac ctg acc acc gcc cag gcc aac atc ggc atg gaa ctt	499
Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn Ile Gly Met Glu Leu	
	120 125 130

gat cgc tcc gta tcc cct tgt acc gtc aac gct gtt gag cac atg gct	547
Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala Val Glu His Met Ala	
	135 140 145

tcc gag gcc tac tac aac gat act gtc tgc cac cgc atc acc acc tct	595
Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His Arg Ile Thr Thr Ser	
	150 155 160 165

ggc att tac gtt ctc cag tgc gcc gat cca agc agc acc ggc gca gcc	643
Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser Ser Thr Gly Ala Gly	
	170 175 180

ggc cca ggg ttc agc ttc gcc aac gaa tac cca acc gac gaa gca act	691
Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro Thr Asp Glu Ala Thr	
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gac cta acc acc cca gtc atc tac gag cgc gcc acc atc gcc atg gcc	739
Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly Thr Ile Ala Met Ala	

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Thr Ile Ala Met Ala Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val
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Leu Pro Gln Leu Arg Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu
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Ser Trp His

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gtc tgg aaa gcc gcc acc gaa gaa gca gaa ctc ctc gca gct gac ggc 96
Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
20 25 30

gcc gtc cac gac cag gaa ctc ttc ctc aac tgc acc acc tcc cca ctg 144
Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
35 40 45

atc ttc gcc tcc gcg atg ctc aac ttc ggc gtc cac caa atc ctg gac 192
Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
50 55 60

acc ctc tgc caa ctc gca cca tcc ccc gcc ggc cgc gac gca gac ccc 240
Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro
65 70 75 80

aaa gcc ctc gaa gcc gcc acc tcc gca atg gac gac cac cgc gac acc 288
Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr
85 90 95

acc gac gac ttc tcc ggc gtc gtc ttc aaa gtc caa gcc ggc atg gac 336
Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp
100 105 110

aaa aac cac cgc gat acc ctc gcc ttc atg cgc gtc gtc tcc gcc gaa 384
Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu
115 120 125

ttc gac cgc ggc atg caa gtc acc cac tcc caa tcc ggc cgc agc ttc 432
Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe
130 135 140

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tcc acc aaa tac gcc ctc acc gtc ttc ggc cgc acc cgc tct acc gtc 480
 Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val
 145 150 155 160

gaa acc gcc ttc ccc ggc gac atc gtc ggc ctc gtc aac gcc ggc gcc 528
 Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala
 165 170 175

ctc gca cca ggc gac acc atc ttc gaa ggc cga aaa atc caa tac cca 576
 Leu Ala Pro Gly Asp Thr Ile Phe Gly Arg Lys Ile Gln Tyr Pro
 180 185 190

cca atg cca aaa ttc gcg cca gaa cac ttc cgc atc ctg cgc gcc aaa 624
 Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys
 195 200 205

tca ctc ggc aaa tac aaa cag ttc cgc aaa gcc ctc gag cag ctg gac 672
 Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
 210 215 220

tcc gaa ggt gtc gtc cag atc ctc aag aac gac ctg cgt ggc gac gcc 720
 Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala
 225 230 235 240

aac cca ggt cat ggc cgg tgt 741
 Asn Pro Gly His Gly Arg Cys
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<210> 76
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 <213> *Corynebacterium glutamicum*
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 20 25 30
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 35 40 45
 Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
 50 55 60
 Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro
 65 70 75 80
 Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr
 85 90 95
 Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp
 100 105 110
 Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu
 115 120 125
 Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe
 130 135 140

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Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val
 145 150 155 160

Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala
 165 170 175

Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro
 180 185 190

Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys
 195 200 205

Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
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Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala
 225 230 235 240

Asn Pro Gly His Gly Arg Cys
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(478)
 <223> RXN02002

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 Met Ser Asn Ala Asn
 1 5

tcc gac acc acc gcc gcc gag gca cat cgc cgc aga aca ttc gcc gta 163
 Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg Arg Thr Phe Ala Val
 10 15 20

atc gca cac ccc gac gcc ggt aaa tcc acc etc acc gag gca ttg gcg 211
 Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu Thr Glu Ala Leu Ala
 25 30 35

ctg cat gca cac atc atc tcc gaa gcc ggc gcc acc cac ggc aaa gca 259
 Leu His Ala His Ile Ile Ser Glu Ala Gly Ala Thr His Gly Lys Ala
 40 45 50

ggc cgc aaa gcc acc gtt tcc gac tgg atg gaa atg gaa aaa gac cgc 307
 Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu Met Glu Lys Asp Arg
 55 60 65

ggc atc tcc atc gcc tcc tcc gca etc caa ttc gag tac gca cca gaa 355
 Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe Glu Tyr Ala Pro Glu
 70 75 80 85

ggc cac gca ggc gag ccc ttc atg atc aac etc gtg gac acc cca ggc 403

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Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu Val Asp Thr Pro Gly
 90 95 100

cac gcc gac ttc tcc gaa gac acc tac cgc gtc ctc atg gcc gtc gac 451
 His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val Leu Met Ala Val Asp
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gca gca gtc atg ctt atg cac tcc gtc 478
 Ala Ala Val Met Leu Met His Ser Val
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<210> 78
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<400> 78
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Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser Glu Ala Gly Ala
 35 40 45

Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu
 50 55 60

Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe
 65 70 75 80

Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu
 85 90 95

Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val
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Leu Met Ala Val Asp Ala Ala Val Met Leu Met His Ser Val
 115 120 125

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 <212> DNA
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 <223> RXN02736

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acgggtcacac ctggcgacagg ccataattta ggggcaaaaa atg atc ttt gaa ctt 115
 Met Ile Phe Glu Leu
 1 5

cgg gat acc acc acc cag caa att tcc aag acc cta act cga ctg cgt 163

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gaa	tcg	ggc	acc	cag	gtc	acc	acc	ggc	cga	gtg	ctc	acc	ctc	atc	gtg	211
Glu	Ser	Gly	Thr	Gln	Val	Thr	Thr	Gly	Arg	Val	Leu	Thr	Leu	Ile	Val	
			25					30					35			
gtc	act	gac	tcc	gaa	agc	gat	gtc	gct	gca	gtt	acc	gag	tcc	acc	aat	259
Val	Thr	Asp	Ser	Glu	Ser	Asp	Val	Ala	Ala	Val	Thr	Glu	Ser	Thr	Asn	
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gaa	gcc	tcg	cgc	gag	cac	cca	tct	cgc	gtg	atc	att	ttg	gtg	gtt	ggc	307
Glu	Ala	Ser	Arg	Glu	His	Pro	Ser	Arg	Val	Ile	Ile	Leu	Val	Val	Gly	
		55				60					65					
gat	aaa	act	gca	gaa	aac	aaa	gtt	gac	gca	gaa	gtc	cgt	atc	ggg	ggc	355
Asp	Lys	Thr	Ala	Glu	Asn	Lys	Val	Asp	Ala	Glu	Val	Arg	Ile	Gly	Gly	
	70				75					80				85		
gac	gct	ggg	gct	tcc	gag	atg	atc	atc	atg	cat	ctc	aac	gga	cct	gtc	403
Asp	Ala	Gly	Ala	Ser	Glu	Met	Ile	Ile	Met	His	Leu	Asn	Gly	Pro	Val	
				90					95					100		
gct	gac	aag	ctc	cag	tat	gtc	gtc	aca	cca	ctg	ttg	ctt	cct	gac	acc	451
Ala	Asp	Lys	Leu	Gln	Tyr	Val	Val	Thr	Pro	Leu	Leu	Leu	Pro	Asp	Thr	
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Pro	Ile	Val	Ala	Trp	Trp	Pro	Gly	Glu	Ser	Pro	Lys	Asn	Pro	Ser	Gln	
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gac	cca	att	gga	cgc	atc	gca	caa	cga	cgc	atc	act	gat	gct	ttg	tac	547
Asp	Pro	Ile	Gly	Arg	Ile	Ala	Gln	Arg	Arg	Ile	Thr	Asp	Ala	Leu	Tyr	
		135				140					145					
gac	cgt	gat	gac	gca	cta	gaa	gat	cgt	gtt	gag	aac	tat	cac	cca	ggg	595
Asp	Arg	Asp	Asp	Ala	Leu	Glu	Asp	Arg	Val	Glu	Asn	Tyr	His	Pro	Gly	
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Asp	Thr	Asp	Met	Thr	Trp	Ala	Arg	Leu	Thr	Gln	Trp	Arg	Gly	Leu	Val	
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gcc	tcc	tca	ttg	gat	cac	cca	cca	cac	agc	gaa	atc	act	tcc	gtg	agg	691
Ala	Ser	Ser	Leu	Asp	His	Pro	Pro	His	Ser	Glu	Ile	Thr	Ser	Val	Arg	
			185					190					195			
ctg	acc	ggg	gca	agc	ggc	agt	acc	tcg	gtg	gat	ttg	gct	gca	ggc	tgg	739
Leu	Thr	Gly	Ala	Ser	Gly	Ser	Thr	Ser	Val	Asp	Leu	Ala	Ala	Gly	Trp	
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Leu	Ala	Arg	Arg	Leu	Lys	Val	Pro	Val	Ile	Arg	Glu	Val	Thr	Asp	Ala	
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ccc	acc	gtg	cca	acc	gat	gag	ttt	ggg	act	cca	ctg	ctg	gct	atc	cag	835
Pro	Thr	Val	Pro	Thr	Asp	Glu	Phe	Gly	Thr	Pro	Leu	Leu	Ala	Ile	Gln	
		230			235					240				245		
cgc	ctg	gag	atc	gtt	cgc	acc	acc	ggc	tcg	atc	atc	atc	acc	atc	tat	883
Arg	Leu	Glu	Ile	Val	Arg	Thr	Thr	Gly	Ser	Ile	Ile	Ile	Thr	Ile	Tyr	

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250										255										260										
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Asp Ala His Thr Leu Gln Val Glu Met Pro Glu Ser Gly Asn Ala Pro																														
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tcg ctg gtg gct att ggt cgt cga agt gag tcc gac tgc ttg tct gag	979																													
Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser Asp Cys Leu Ser Glu																														
280	285	290																												
gag ctt cgc cac atg gat cca gat ttg ggc tac cag cac gca cta tcc	1027																													
Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr Gln His Ala Leu Ser																														
295	300	305																												
ggc ttg tcc agc gtc aag ctg gaa acc gtc taaggagaaaa tacaacacta	1077																													
Gly Leu Ser Ser Val Lys Leu Glu Thr Val																														
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Leu Thr Leu Ile Val Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val																														
35	40	45																												
Thr Glu Ser Thr Asn Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile																														
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Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu																														
65	70	75	80																											
Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His																														
85	90	95																												
Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu																														
100	105	110																												
Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro																														
115	120	125																												
Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile																														
130	135	140																												
Thr Asp Ala Leu Tyr Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu																														
145	150	155	160																											
Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln																														
165	170	175																												
Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu																														

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180 185 190

Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp
195 200 205

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210 215 220

Glu Val Thr Asp Ala Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro
225 230 235 240

Leu Leu Ala Ile Gln Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile
245 250 255

Ile Ile Thr Ile Tyr Asp Ala His Thr Leu Gln Val Glu Met Pro Glu
260 265 270

Ser Gly Asn Ala Pro Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser
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Met Ala Gln Gly Thr
1 5

gtg aaa tgg ttc aac ggc gaa aag gga ttt ggt ttc atc gct ccc aac 163
Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Ile Ala Pro Asn
10 15 20

gat ggc tcc gca gat ctc ttc gtc cac tac tct gag att cag ggc tcc 211
Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser Glu Ile Gln Gly Ser
25 30 35

ggt ttc cgt aat ctt gag gaa aac cag cca gtt gaa ttt gag gtc ggc 259
Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val Glu Phe Glu Val Gly
40 45 50

gag ggc gcc aag ggc cca cag gct cag cag gtt cgt gct ctc 301
Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val Arg Ala Leu
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taagctctaa ctgctagcta aaaattccgc 331

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<210> 82
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 35 40 45

 Glu Phe Glu Val Gly Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val
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 Arg Ala Leu
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 <210> 83
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 Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly Phe Ile Ala Pro Asn
 10 15 20

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 Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser Glu Ile Gln Gly Ser
 25 30 35

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 Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val Glu Phe Glu Val Gly
 40 45 50

 gag ggc gcc aag ggc cca cag gct cag cag gtt cgt gct ctg 301
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 Val Pro Val Gly Thr
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 Val Lys Trp Tyr Asp Ala Glu Arg Gly Phe Gly Phe Val Ser Asn Pro
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 Gly Gly Glu Asp Cys Phe Val Gly Lys Gln Val Leu Pro Lys Gly Val
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 acc gaa ttg cac aag gga cag cga atc gat ttt gac ttc gcc gca ggc 259
 Thr Glu Leu His Lys Gly Gln Arg Ile Asp Phe Asp Phe Ala Ala Gly
 40 45 50
 cgt aag ggc cct caa gca ctt cga ata aag att ctt gaa act cca cgc 307
 Arg Lys Gly Pro Gln Ala Leu Arg Ile Lys Ile Leu Glu Thr Pro Arg
 55 60 65
 agg cgt cca cag cac aaa tac aag cca gaa gag ctc aac gga atg atc 355
 Arg Arg Pro Gln His Lys Tyr Lys Pro Glu Glu Leu Asn Gly Met Ile
 70 75 80 85
 tct gac ctc atc acg ctt cta gaa agt gga gtg caa cca ggc ctt gcc 403
 Ser Asp Leu Ile Thr Leu Leu Glu Ser Gly Val Gln Pro Gly Leu Ala
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 Lys Gly Gln Tyr Pro Glu His Lys Ala Gly Ala Gln Val Ala Glu Ile
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 35 40 45

Asp Phe Ala Ala Gly Arg Lys Gly Pro Gln Ala Leu Arg Ile Lys Ile
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Leu Glu Thr Pro Arg Arg Arg Pro Gln His Lys Tyr Lys Pro Glu Glu
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Leu Asn Gly Met Ile Ser Asp Leu Ile Thr Leu Leu Glu Ser Gly Val
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 Asp Gly Ser Ala Asp Val Phe Val His Tyr Ser Glu Ile Glu Gly Asn
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 Gly Phe Arg Thr Leu Glu Glu Asn Gln Leu Val Glu Phe Glu Ile Gly
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 Met Asp Asn Gly Trp
 1 5

cag aac ctg caa act ctc gca ctc ttt gtg gcg att gtg gaa gag ggg 163
 Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala Ile Val Glu Glu Gly
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 Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met Ala Gln Pro Asn Ala
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 Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met Lys Ala Glu Leu Leu
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 Val Arg His Pro Arg Gly Ser His Pro Thr Ala Ala Gly Leu Ala Leu
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 Val Glu His Ser Arg Asp Leu Leu Gln Ser Val Gln Glu Phe Thr Glu
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 Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu Lys Leu His Val Gly
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 Phe Ile Glu Thr Pro His Val Pro Val Arg Leu His Ala Arg Val Val
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 170 175 180

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 185 190 195

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 215 220 225

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 Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly Glu Leu Val Ser Ile
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 Val Ser Val Met Asn Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly
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 His Ala Arg Val Val Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro
 165 170 175
 Asn His Glu Trp Ala Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu
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1201

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Ser Gly Leu Gly Trp Met Ala Asn Leu Arg Phe Gly Val Ser Arg Met	135 140 145	
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295															300	305				
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Arg	Leu	Ala	Thr	Val	Pro	Ala	Pro	Glu	Pro	Ala	Ile	Ile	Arg	Val	Arg					
310															315	320				
cat	gaa	att	gat	cca	ggc	gaa	gaa	gtc	tcc	caa	tct	gct	cga	aaa	gtg	1123				
His	Glu	Ile	Asp	Pro	Gly	Glu	Glu	Val	Ser	Gln	Ser	Ala	Arg	Lys	Val					
330															335	340				
ggc	att	gga	gtg	gcc	gtg	ggc	gcc	act	gcg	ggc	ggt	gct	ttt	gcg	ctg	1171				
Gly	Ile	Gly	Val	Ala	Val	Gly	Ala	Ala	Thr	Ala	Gly	Ala	Phe	Ala	Leu					
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Leu	Arg	Lys	Lys																	
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Asp Lys His Asp Trp Phe Asp His Leu Met Arg Met Asn Glu Arg Phe																				

35	40	45
Gly Ala Lys Gly Gly Asn Gln Leu Ser Ala Gly Ile Thr Tyr Phe Ser	55	60
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Val Leu Ser Ile Phe Pro Ile Ala Met Leu Val Phe Gly Ile Ala Gly	70	80
65		
Val Ile Leu Ala Gly Asn Pro Glu Val Leu Thr Asp Ile Gln Asn Arg	85	95
Ile Asn Asp Ala Leu Glu Gly Glu Ile Gly Asn Thr Val Asn Gly Ile	105	110
100		
Ile Asp Ser Ala Ile Ala Gln Arg Gly Ala Val Leu Gly Ile Gly Gly	120	125
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Val Thr Ala Leu Trp Ser Gly Leu Gly Trp Met Ala Asn Leu Arg Phe	135	140
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Gly Val Ser Arg Met Trp Ala Ile Asp Pro Thr Glu Gly Asn Phe Ile	150	155
145		
Gln Lys Lys Leu Thr Asp Leu Val Ala Leu Ile Val Leu Leu Leu Ala	165	170
		175
Met Gly Val Ala Phe Gly Ile Thr Ala Leu Gly Ala Ser Gly Leu Thr	180	185
		190
Lys Asn Leu Leu Asp Phe Val Gly Leu Gly Glu Ile Pro Gly Ile Ser	195	200
		205
Tyr Ile Thr Trp Val Val Ala Ala Leu Val Gly Val Leu Ala Asn Phe	210	215
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Leu Val Phe Met Trp Leu Ile Phe Ser Leu Pro Arg Thr Lys Val Pro	225	230
		235
Met Lys Pro Gly Leu Gln Ala Ala Leu Leu Gly Ala Ile Gly Phe Glu	245	250
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Val Val Lys Gln Val Gly Ser Leu Leu Ala Ser Asn Ala Leu Ser Asn	260	265
		270
Pro Ala Gly Ala Ala Phe Gly Pro Ile Ile Gly Ile Met Val Val Leu	275	280
		285
Tyr Leu Ile Trp Arg Ile Leu Met Tyr Cys Ser Ala Trp Ala Ala Thr	290	295
		300
Ser Glu Glu Ala Leu Arg Leu Ala Thr Val Pro Ala Pro Glu Pro Ala	305	310
		315
Ile Ile Arg Val Arg His Glu Ile Asp Pro Gly Glu Glu Val Ser Gln	325	330
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Ser Ala Arg Lys Val Gly Ile Gly Val Ala Val Gly Ala Ala Thr Ala	340	345
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cca gcg	ccc gag	aat ctc	ctg gac	gcc gag	aga att	cag atg	atc aag	163	
Pro Ala	Pro Glu	Asn 10	Leu Leu	Asp Ala	Glu Arg	Ile Gln	Met Ile	Lys 20	
aac ttc	cgc aac	gaa tta	acg ggg	ttc atg	ctc aac	tac caa	ttt ggc	211	
Asn Phe	Arg Asn	Glu Leu	Thr Gly	Phe Met	Leu Asn	Tyr Gln	Phe Gly	35	
att gat	gag atc	ctg acc	aag atc	aac atc	ctg aaa	act gaa	ttc agc	259	
Ile Asp	Glu Ile	Leu Thr	Lys Ile	Asn Ile	Leu Lys	Thr Glu	Phe Ser	40	
cag ctg	cac gaa	tac gca	cct atc	gag cac	gta tct	tca cga	ttg aag	307	
Gln Leu	His Glu	Tyr Ala	Pro Ile	Glu His	Val Ser	Ser Arg	Leu Lys	55	
aca cca	gaa agc	atc gtc	aaa aag	gtc atc	cga aaa	gga gac	gag ctc	355	
Thr Pro	Glu Ser	Ile Val	Lys Lys	Val Ile	Arg Lys	Gly Asp	Glu Leu	70	
tcc ctc	gca gct	atc aaa	gac aca	gtg ttt	gat atc	gca ggc	att cga	403	
Ser Leu	Ala Ala	Ile Lys	Asp Thr	Val Phe	Asp Ile	Ala Gly	Ile Arg	90	
atc gtc	tgc agt	ttc ctc	aaa gat	gcc atc	tac gca	atc gcc	gat atg	451	
Ile Val	Cys Ser	Phe Leu	Lys Asp	Ala Tyr	Ala Ala	Ile Ala	Asp Met	Leu 105	
acc aac	caa aaa	gac gtc	acg gtc	atc gag	gcc aaa	gac tac	atc gct	499	
Thr Asn	Gln Lys	Asp Val	Thr Val	Ile Val	Glu Ala	Lys Asp	Tyr Ile	120	
aac cca	aag ccg	aac ggc	tac aag	agt ttg	cac ctt	atc ctc	caa gtg	547	
Asn Pro	Lys Pro	Asn Gly	Tyr Lys	Ser Leu	His Leu	Ile Leu	Gln Val	135	
cct gtc	ttc ctg	tct aac	tcc gtg	gaa aag	gtc val	asn aat	gtt gaa	595	
Pro Val	Phe Leu	Ser Asn	Ser Val	Glu Lys	Val Asn	Val Glu	Val Gln	150	
atc cgc	acc att	gcc atg	gac ttc	tgg gca	agc ctc	gag cac	aaa atc	643	
Ile Arg	Thr Ile	Ala Met	Asp Phe	Trp Ala	Ser Leu	Glu His	Lys Ile		


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                170                175                180
tac tac aaa ttt gaa caa gaa gtt cct cag tca atc ctt gat gag ctg 691
Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu
                185                190                195

agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740
Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu Val Thr
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gttgaaacca ctg 753

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Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu
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Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val
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Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg
                65                70                75                80

Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp
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Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala
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Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala
                115                120                125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His
                130                135                140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val
                145                150                155                160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser
                165                170                175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser
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Val Thr
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 Met Ser Ser Pro Val
 1 5
 atc agc ccc gaa acc aaa acc gga aag aag atc ctg ctt gca gcc cct 163
 Ile Ser Pro Glu Thr Lys Thr Gly Lys Lys Ile Leu Leu Ala Ala Pro
 10 15 20
 cgc gga tac tgt gcc ggc gta gac cgt gca gtg gaa acc gtc gag cgc 211
 Arg Gly Tyr Cys Ala Gly Val Asp Arg Ala Val Glu Thr Val Glu Arg
 25 30 35
 gcg ctc gag gaa tac ggc gcc cca att tat gtc cgt aaa gaa atc gtg 259
 Ala Leu Glu Glu Tyr Gly Ala Pro Ile Tyr Val Arg Lys Glu Ile Val
 40 45 50
 cac aac cgt tac gtt gtg gac acc ctg gca gaa aag ggc gcg att ttt 307
 His Asn Arg Tyr Val Val Asp Thr Leu Ala Glu Lys Gly Ala Ile Phe
 55 60 65
 gtc aac gaa gca tct gaa gca cca gaa ggt gcc aac atg gtg ttc tct 355
 Val Asn Glu Ala Ser Glu Ala Pro Glu Gly Ala Asn Met Val Phe Ser
 70 75 80 85
 gca cac ggc gtg agc cca atg gtc cac gaa gaa gct gca gct aaa aac 403
 Ala His Gly Val Ser Pro Met Val His Glu Glu Ala Ala Ala Lys Asn
 90 95 100
 atc aag gct att gac gcg gcc tgc ccg ctg gtc acc aaa gtg cac aag 451
 Ile Lys Ala Ile Asp Ala Ala Cys Pro Leu Val Thr Lys Val His Lys
 105 110 115
 gaa gtc cag cgc ttt gat aag cag gga ttc cac att ctc ttc atc ggt 499
 Glu Val Gln Arg Phe Asp Lys Gln Gly Phe His Ile Leu Phe Ile Gly
 120 125 130
 cac gaa ggc cat gaa gaa gta gag ggc acc atg ggt cat tcc gtt gag 547
 His Glu Gly His Glu Glu Val Glu Gly Thr Met Gly His Ser Val Glu
 135 140 145
 aaa acc cac ctg gtt gac ggc gtt gct ggc att gcc acc ctg cct gaa 595
 Lys Thr His Leu Val Asp Gly Val Ala Gly Ile Ala Thr Leu Pro Glu
 150 155 160 165
 ttc tta aac gat gaa cca aac ctg atc tgg ctg tct cag acc acg ctt 643
 Phe Leu Asn Asp Glu Pro Asn Leu Ile Trp Leu Ser Gln Thr Thr Leu
 170 175 180

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Ser	Val	Asp	Leu	Thr	Met	Glu	Ile	Val	Arg	Glu	Leu	Lys	Val	Lys	Phe	
		185						190					195			
cct	cag	ctg	cag	gat	cca	ccg	tca	gat	gat	att	tgc	tac	gcc	acg	cag	739
Pro	Gln	Leu	Gln	Asp	Pro	Pro	Ser	Asp	Asp	Ile	Cys	Tyr	Ala	Thr	Gln	
		200					205					210				
aac	cgc	cag	gtt	gcc	gtc	aag	gct	atc	gct	gag	cgc	tgc	gag	ctg	atg	787
Asn	Arg	Gln	Val	Ala	Val	Lys	Ala	Ile	Ala	Glu	Arg	Cys	Glu	Leu	Met	
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att	gtg	gtc	ggt	tcc	cgc	aac	tcc	tcc	aac	tcg	gtt	cgt	ctg	gtt	gag	835
Ile	Val	Val	Gly	Ser	Arg	Asn	Ser	Ser	Asn	Ser	Val	Arg	Leu	Val	Glu	
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gtc	gct	aag	caa	aac	ggt	gcc	gat	aac	gcc	tac	ctg	gtg	gat	tac	gcc	883
Val	Ala	Lys	Gln	Asn	Gly	Ala	Asp	Asn	Ala	Tyr	Leu	Val	Asp	Tyr	Ala	
				250					255					260		
cgc	gaa	atc	gac	cca	gca	tgg	ttc	gaa	ggc	gta	gag	acc	atc	ggg	atc	931
Arg	Glu	Ile	Asp	Pro	Ala	Trp	Phe	Glu	Gly	Val	Glu	Thr	Ile	Gly	Ile	
			265					270					275			
tcc	tcc	ggc	gct	tcc	gtg	cct	gag	atc	ctc	gtc	cag	ggc	gtc	att	gag	979
Ser	Ser	Gly	Ala	Ser	Val	Pro	Glu	Ile	Leu	Val	Gln	Gly	Val	Ile	Glu	
		280					285					290				
cgc	ctg	gct	gag	ttc	ggc	tac	gac	gac	gtc	gag	gaa	gtc	acc	tcc	gcc	1027
Arg	Leu	Ala	Glu	Phe	Gly	Tyr	Asp	Asp	Val	Glu	Glu	Val	Thr	Ser	Ala	
		295				300					305					
gct	gag	aag	att	gtt	ttc	gcg	ctg	cct	cgc	gtg	ctg	cgc	cac	aag	aat	1075
Ala	Glu	Lys	Ile	Val	Phe	Ala	Leu	Pro	Arg	Val	Leu	Arg	His	Lys	Asn	
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Leu	Leu															

Asn Met Val Phe Ser Ala His Gly Val Ser Pro Met Val His Glu Glu
 85 90 95
 Ala Ala Ala Lys Asn Ile Lys Ala Ile Asp Ala Ala Cys Pro Leu Val
 100 105 110
 Thr Lys Val His Lys Glu Val Gln Arg Phe Asp Lys Gln Gly Phe His
 115 120 125
 Ile Leu Phe Ile Gly His Glu Gly His Glu Glu Val Glu Gly Thr Met
 130 135 140
 Gly His Ser Val Glu Lys Thr His Leu Val Asp Gly Val Ala Gly Ile
 145 150 155 160
 Ala Thr Leu Pro Glu Phe Leu Asn Asp Glu Pro Asn Leu Ile Trp Leu
 165 170 175
 Ser Gln Thr Thr Leu Ser Val Asp Glu Thr Met Glu Ile Val Arg Glu
 180 185 190
 Leu Lys Val Lys Phe Pro Gln Leu Gln Asp Pro Pro Ser Asp Asp Ile
 195 200 205
 Cys Tyr Ala Thr Gln Asn Arg Gln Val Ala Val Lys Ala Ile Ala Glu
 210 215 220
 Arg Cys Glu Leu Met Ile Val Val Gly Ser Arg Asn Ser Ser Asn Ser
 225 230 235 240
 Val Arg Leu Val Glu Val Ala Lys Gln Asn Gly Ala Asp Asn Ala Tyr
 245 250 255
 Leu Val Asp Tyr Ala Arg Glu Ile Asp Pro Ala Trp Phe Glu Gly Val
 260 265 270
 Glu Thr Ile Gly Ile Ser Ser Gly Ala Ser Val Pro Glu Ile Leu Val
 275 280 285
 Gln Gly Val Ile Glu Arg Leu Ala Glu Phe Gly Tyr Asp Asp Val Glu
 290 295 300
 Glu Val Thr Ser Ala Ala Glu Lys Ile Val Phe Ala Leu Pro Arg Val
 305 310 315 320
 Leu Arg His Lys Asn
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<212> DNA

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<223> RXS01027

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Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp Glu Leu Gly Leu Asp
230          235          240          245

gtg tcc gtc aac cga ctg ttc ggc gac gac gcc tgg gaa acc gat ccc 883
Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro
          250          255          260

gag gcc tgc aag aag gcg ttc acc gac gtg gtc gcg caa ggt ggc gtg 931
Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val
          265          270          275

cgg atg atc gtt ggg cag ggc gac atc att ccg gaa atg atc aaa tgg 979
Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp
          280          285          290

ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa 1027
Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys
          295          300          305

aag gcc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc 1075
Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly
310          315          320          325

gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg ttttaaggcct 1128
Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
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cca 1131

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Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp
          35          40          45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
          50          55          60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
          65          70          75          80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
          85          90          95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
          100          105          110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
          115          120          125

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Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
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 Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
 145 150 155 160
 Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
 165 170 175
 Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
 180 185 190
 Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
 195 200 205
 Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr
 210 215 220
 Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp
 225 230 235 240
 Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala
 245 250 255
 Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val
 260 265 270
 Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro
 275 280 285
 Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu
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 305 310 315 320
 Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
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 Val Asn Gln Ala Trp
 1 5
 cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163

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 Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp
 25 30 35
 ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259
 Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly
 40 45 50
 cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307
 Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Glu Pro Gly Glu Asp
 55 60 65
 aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac 355
 Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His
 70 75 80 85
 ggt gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg 403
 Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser
 90 95 100
 gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat 451
 Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr
 105 110 115
 gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg 499
 Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala
 120 125 130
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 Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu
 135 140 145
 cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg 595
 Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu
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 aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaaccg 648
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 aac 651

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 35 40 45

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Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
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 Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
 65 70 75 80
 Glu Thr Gly Ile His Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp
 85 90 95
 Tyr Trp Phe Val Ser Glu Gly Lys Arg Ile His Lys Thr Val His His
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 His Leu Leu Arg Tyr Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu
 115 120 125
 Val Thr Glu Val Ala Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu
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 Val Arg Leu Gly Lys Gly Val Asp Ala Thr Gly Gln Leu Asp Pro Glu
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 Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met
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 Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr
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 Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu
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 Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu

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Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu			
100	105	110	
gac caa ggt cct ttc tgt gtt atc gac ctt ggc ggt gga tcc act gag			384
Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Ser Thr Glu			
115	120	125	
ttc atc gtt ggc acc tac gac ggt gaa atc cta ggc tcc cac tca acc			432
Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr			
130	135	140	
caa atg gga tgc gtg cgc ctg acc gaa cga atc atg cgc agc gac cca			480
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Pro Asp			

<210> 106
 <211> 162
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 106
 Glu Val Thr Pro Glu Gly Phe Lys Glu Ile Thr Arg Glu Asn Thr Ile
 1 5 10 15
 Val Arg Leu Gly Lys Gly Val Asp Ala Thr Gly Gln Leu Asp Pro Glu
 20 25 30
 Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met
 35 40 45
 Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr
 50 55 60
 Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu
 65 70 75 80
 Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu
 85 90 95
 Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu
 100 105 110
 Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Gly Ser Thr Glu
 115 120 125
 Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr
 130 135 140
 Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro
 145 150 155 160
 Pro Asp

00603208-062300

```
<210> 107
<211> 654
<212> DNA
<213> Corynebacterium glutamicum
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```
<220>
<221> CDS
<222> (101)..(631)
<223> RXS01835
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400> 107																		
tcaacatceta	ttctctctgc	gatttgc	catg	ggatatata	t	taaaaaattct	agccgaaagt	60										
ttctctgcgtg	aatacac	ttt	ccccgcgcct	tcgcaaagct	atg	aat	act	gcc	gcg	115								
					Met	Asn	Thr	Ala	Ala	5								
tggtg	gca	cac	cgc	cac	cac	gta	cgc	aaa	ggc	ggg	gga	att	ccg	tat	gtc	163		
Trp	Ala	His	Arg	His	His	Val	Arg	Lys	Gly	Gly	Ile	Pro	Tyr	Val		20		
agg	cat	ctt	tat	tca	gtg	atg	tac	ttg	ctg	gcc	agc	gtc	act	aat	gat	211		
Ser	His	Leu	Tyr	Ser	Val	Met	Tyr	Leu	Leu	Ala	Ser	Val	Thr	Asn	Asp	35		
gaa	gat	gtg	ctc	atc	gcc	ggg	ctg	ctc	cac	gac	acc	ctc	gaa	gac	gta	259		
Glu	Asp	Val	Leu	Ile	Ala	Gly	Leu	Leu	His	Asp	Thr	Leu	Glu	Asp	Val	40		
ccc	gag	gaa	tac	aat	tct	gcc	caa	ctt	gaa	gct	gat	ttt	ggg	ccg	cgg	307		
Pro	Glu	Glu	Tyr	Asn	Ser	Ala	Gln	Leu	Glu	Ala	Asp	Phe	Gly	Pro	Arg	60		
gtg	cgc	gag	ttg	gtg	gaa	gag	ctc	acc	aaa	cag	ccc	tta	aaa	agc	tgg	355		
Val	Arg	Glu	Leu	Val	Glu	Glu	Leu	Thr	Lys	Gln	Pro	Leu	Lys	Ser	Trp	75	85	
aaa	gcg	cgt	gcc	gac	gct	tac	ctc	ctg	cac	ctc	agc	gca	ggt	gcc	agc	403		
Lys	Ala	Arg	Ala	Asp	Ala	Tyr	Leu	Leu	His	Leu	Ser	Ala	Gly	Ala	Ser	90	100	
tta	gag	gct	gtc	tta	atc	tcc	acc	gca	gat	aaa	ctg	cat	aat	ctc	atg	451		
Leu	Glu	Ala	Val	Leu	Ile	Ser	Thr	Ala	Asp	Lys	Leu	His	Asn	Leu	Met	105	115	
tcc	atc	ttg	gat	gac	ctt	gaa	ata	cac	ggg	gaa	gat	tta	tgg	caa	cgc	499		
Ser	Ile	Leu	Asp	Asp	Leu	Glu	Ile	His	Gly	Glu	Asp	Leu	Trp	Gln	Arg	120	125	
ttt	aac	gct	ggc	aaa	gag	cag	caa	atc	tgg	tgg	tat	agc	gag	gtt	tat	547		
Phe	Asn	Ala	Gly	Lys	Glu	Gln	Gln	Ile	Trp	Trp	Tyr	Ser	Glu	Val	Tyr	135	140	
cag	ata	tct	ctc	cag	cgc	tta	ggy	ttc	aat	gag	ttg	aat	aaa	caa	ctg	595		
Gln	Ile	Ser	Leu	Gln	Arg	Leu	Gly	Phe	Asn	Glu	Leu	Asn	Lys	Gln	Leu	150	155	
ggg	ttg	tg	ctc	gaa	aag	ctc	tta	aag	caa	agc	gcc	taggcgctcg				641		
Gly	Leu	Cys	Val	Glu	Lys	Leu	Leu	Lys	Gln	Ser	Ala							

062300

170

175

gcggcggtcga taa

654

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<210> 108
<211> 177
<212> PRT
<213> Corynebacterium glutamicum
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<400> 108
Met Asn Thr Ala Ala Trp Ala His Arg His His Val Arg Lys Gly Gly
1 5 10 15

Gly Ile Pro Tyr Val Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala
20 25 30

Ser Val Thr Asn Asp Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp
35 40 45

Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala
50 55 60

Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln
65 70 75 80

Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu
85 90 95

Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys
100 105 110

Leu His Asn Leu Met Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu
115 120 125

Asp Leu Trp Gln Arg Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp
130 135 140

Tyr Ser Glu Val Tyr Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu
145 150 155 160

Leu Asn Lys Gln Leu Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser
165 170 175

Ala

```
<210> 109
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1027)
<223> RXS02497
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<400> 109
tcgatgccgc cgctggcgaa gactcgggga aacctaaaaa taccgaagaa gaatttgacc 60

0960323106E2300

gattcacact ttgccaccct agaccgtcta accttttaggt gtg aga tta ggt gta 115
Val Arg Leu Gly Val 5
1

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163
Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg 20
10 15

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211
Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg 35
25 30

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259
Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile 50
40 45

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307
Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Asp Leu Ala Lys Thr 60
55 65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tgc gca gtc cgc tcc 355
Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser 85
70 75 80

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc 403
Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly 100
90 95

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc 451
Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe 115
105 110

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac 499
Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn 130
120 125

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa 547
Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu 145
135 140

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc 595
Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr 165
150 155 160

cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc 643
His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu 180
170 175

ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg 691
Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met 195
185 190

cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc 739
Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe 210
200 205

cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca 787
Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro 225
215 220

cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca 835

09507208.062300

His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala
 230 235 240 245

ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc 883
 Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile
 250 255 260

agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa 931
 Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu
 265 270 275

gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg 979
 Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp
 280 285 290

gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag 1027
 Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu
 295 300 305

taacatttac ccggaagga gtt 1050

<210> 110

<211> 309

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 110

Val Arg Leu Gly Val Leu Asp Val Gly Ser Asn Thr Val His Leu Val
 1 5 10 15

Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp
 20 25 30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
 35 40 45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
 50 55 60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
 65 70 75 80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
 85 90 95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
 100 105 110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
 115 120 125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
 130 135 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
 145 150 155 160

Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
 165 170 175

00603208.062300

Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
 180 185 190
 Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
 195 200 205
 Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
 210 215 220
 Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
 225 230 235 240
 Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
 245 250 255
 Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
 260 265 270
 Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
 275 280 285
 Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile
 290 295 300
 Asp Lys Gly Leu Glu
 305
 <210> 111
 <211> 534
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(511)
 <223> RXS02972
 <400> 111
 acctacgacg gtgaaatcct aggcctccac tcaacccaaa tgggatgcgt gcgcctgacc 60
 gaacgaatca tgcgcagcga cccaccgcgac tgaaaccgaa gtg gaa atc gcc cgc 115
 Val Glu Ile Ala Arg
 1 5
 gac tac gtt gca gaa cgc atc cag gaa gta aaa gcc atc gtc cca att 163
 Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys Ala Ile Val Pro Ile
 10 15 20
 tca aag gca aaa acc ttt gtg gga tgc gca ggc acc ttc acc aca atc 211
 Ser Lys Ala Lys Thr Phe Val Gly Cys Ala Gly Thr Phe Thr Thr Ile
 25 30 35
 tcc gcc tgg gtg caa ggc cta gaa agc tac gac cgc gac gcg atc cac 259
 Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp Arg Asp Ala Ile His
 40 45 50
 ctc tct gca etc aac ttc gat gca ctg cga gtt gtc acc gat gag atc 307
 Leu Ser Ser Ala Leu Asn Phe Asp Ala Leu Arg Val Val Thr Asp Glu Ile
 55 60 65

002290-802E0960

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att tca gaa tca tca tca cag cgc gcc agc aac cca gtt gtt gat cca 355
Ile Ser Glu Ser Ser Ser Ser Gln Arg Ala Ser Asn Pro Val Val Asp Pro
70 75 80 85

ggg cgc gcc gac gtc atc ggt ggc gga tcc gtt gtt gtc caa gca gcg 403
Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val Val Val Gln Ala Ala
90 95 100

atc gac tta gcc tcc aaa gaa gcc ggt gta gac tac atc att att tcc 451
Ile Asp Leu Ala Ser Lys Glu Ala Gly Val Asp Tyr Ile Ile Ile Ser
105 110 115

gaa aaa gac atc ctc gac ggc ctc atc ctt ggc ctg gta gaa gcc gac 499
Glu Lys Asp Ile Leu Asp Gly Leu Ile Leu Gly Leu Val Glu Ala Asp
120 125 130

tct ttg aag aaa taggacctta gttttaaaccc act 534
Ser Leu Lys Lys
135

```

```

<210> 112
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 112
Val Glu Ile Ala Arg Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys
1 5 10 15

Ala Ile Val Pro Ile Ser Lys Ala Lys Thr Phe Val Gly Cys Ala Gly
20 25 30

Thr Phe Thr Thr Ile Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp
35 40 45

Arg Asp Ala Ile His Leu Ser Ala Leu Asn Phe Asp Ala Leu Arg Val
50 55 60

Val Thr Asp Glu Ile Ile Ser Glu Ser Ser Ser Gln Arg Ala Ser Asn
65 70 75 80

Pro Val Val Asp Pro Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val
85 90 95

Val Val Gln Ala Ala Ile Asp Leu Ala Ser Lys Glu Ala Gly Val Asp
100 105 110

Tyr Ile Ile Ile Ser Glu Lys Asp Ile Leu Asp Gly Leu Ile Leu Gly
115 120 125

Leu Val Glu Ala Asp Ser Leu Lys Lys
130 135

```

```

<210> 113
<211> 636
<212> DNA
<213> Corynebacterium glutamicum

<220>

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002290.80220960


```
<210> 114
<211> 171
<212> PRT
<213> Corynebacterium glutamicum
```

Figure 6

<400> 114

Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val
 1 5 10 15

Thr Arg Thr Ala Arg Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln
 20 25 30

Lys Val Thr Ser Gln Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly
 35 40 45

Ile Asp Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly
 50 55 60

Ala Arg Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly
 65 70 75 80

Pro Val Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys
 85 90 95

Leu Arg Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly
 100 105 110

Asn Ile Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala
 115 120 125

Ser Phe Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala
 130 135 140

Gly Asp Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys
 145 150 155 160

Glu Leu Gly Glu Leu Leu Ser Gly Arg Thr Thr
 165 170

<210> 115

<211> 486

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(463)

<223> RXA02201

<400> 115

tctaccagcc aaatcatcaa ctcatagcga aggaatcaac ttcatagaata atcaaccatc 60

agtacttttc gtttgcgtcg gcaatggtgg aaaatctcaa atg gcc gca gcg cta 115
 Met Ala Ala Ala Leu
 1 5

gcc aaa aaa cat gcc ggg gac gct ctc aaa gtt tat tca gct gcc aca 163
 Ala Lys Lys His Ala Gly Asp Ala Leu Lys Val Tyr Ser Ala Gly Thr
 10 15 20

aag cca ggt acg aaa tta aat caa cag tcc ctt gat tcc att gct gaa 211
 Lys Pro Gly Thr Lys Leu Asn Gln Gln Ser Leu Asp Ser Ile Ala Glu
 25 30 35

gtt ggc gca gat atg tct caa ggg ttt cca aag gcc att gac cag gag 259

006290-80260960

Val Gly Ala Asp Met Ser Gln Gly Phe Pro Lys Gly Ile Asp Gln Glu
 40 45 50
 tta att aag cga gta gac cgc gtg gtc att ctt ggt gcc gaa gct caa 307
 Leu Ile Lys Arg Val Asp Arg Val Val Ile Leu Gly Ala Glu Ala Gln
 55 60 65
 cta gaa atg cct atc gat gca aac ggc ata cta cag cgc tgg gta act 355
 Leu Glu Met Pro Ile Asp Ala Asn Gly Ile Leu Gln Arg Trp Val Thr
 70 75 80 85
 gac gaa ccc tct gaa cgt gga att gaa ggt atg gaa cgc atg cgc ctg 403
 Asp Glu Pro Ser Glu Arg Gly Ile Glu Gly Met Glu Arg Met Arg Leu
 90 95 100
 gtc cga gat gat att gac gcc cga gtc caa aac ctc gtc gct gaa cta 451
 Val Arg Asp Asp Ile Asp Ala Arg Val Gln Asn Leu Val Ala Glu Leu
 105 110 115
 acc caa aac gca tagcagtttt ctaatctcac aca 486
 Thr Gln Asn Ala
 120
 <210> 116
 <211> 121
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 116
 Met Ala Ala Ala Leu Ala Lys Lys His Ala Gly Asp Ala Leu Lys Val
 1 5 10 15
 Tyr Ser Ala Gly Thr Lys Pro Gly Thr Lys Leu Asn Gln Gln Ser Leu
 20 25 30
 Asp Ser Ile Ala Glu Val Gly Ala Asp Met Ser Gln Gly Phe Pro Lys
 35 40 45
 Gly Ile Asp Gln Glu Leu Ile Lys Arg Val Asp Arg Val Val Ile Leu
 50 55 60
 Gly Ala Glu Ala Gln Leu Glu Met Pro Ile Asp Ala Asn Gly Ile Leu
 65 70 75 80
 Gln Arg Trp Val Thr Asp Glu Pro Ser Glu Arg Gly Ile Glu Gly Met
 85 90 95
 Glu Arg Met Arg Leu Val Arg Asp Asp Ile Asp Ala Arg Val Gln Asn
 100 105 110
 Leu Val Ala Glu Leu Thr Gln Asn Ala
 115 120
 <210> 117
 <211> 510
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>

00602200.002300

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<221> CDS
<222> (101)..(487)
<223> RXA00599
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[illegible]

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<210> 118
<211> 129
<212> PRT
<213> Corvnebacterium glutamicum
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<400> 118
Met Lys Ser Val Leu Phe Val Cys Val Gly Asn Gly Gly Lys Ser Gln
  1              5              10              15
Met Ala Ala Ala Leu Ala Gln Lys Tyr Ala Ser Asp Ser Val Glu Ile
  20              25              30
His Ser Ala Gly Thr Lys Pro Ala Gln Gly Leu Asn Gln Leu Ser Val
  35              40              45

```

0530F0530F

Glu Ser Ile Ala Glu Val Gly Ala Asp Met Ser Gln Gly Ile Pro Lys
 50 55 60
 Ala Ile Asp Pro Glu Leu Leu Arg Thr Val Asp Arg Val Val Ile Leu
 65 70 75 80
 Gly Asp Asp Ala Gln Val Asp Met Pro Glu Ser Ala Gln Gly Ala Leu
 85 90 95
 Glu Arg Trp Ser Ile Glu Glu Pro Asp Ala Gln Gly Met Glu Arg Met
 100 105 110
 Arg Ile Val Arg Asp Gln Ile Asp Asn Arg Val Gln Ala Leu Leu Ala
 115 120 125
 Gly

<210> 119
 <211> 1221
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1198)
 <223> RXA00600

<400> 119
 cggagttaat gagcggtagg tggatgggtg cggtcatgtc cgctcattata tattgacgca 60
 catcgatatt gaagggtattt ttatatcggc aaacatcaat atg att gaa ggc tgg 115
 Met Ile Glu Gly Trp
 1 5
 ctc atg acc ctt act aaa gag cat tcg aca cct cga gcg gct ggc tca 163
 Leu Met Thr Leu Thr Lys Glu His Ser Thr Pro Arg Ala Ala Gly Ser
 10 15 20
 atg tcg ttt ctt gac cgc tgg tta gct gcc tgg att ttc ttg gct atg 211
 Met Ser Phe Leu Asp Arg Trp Leu Ala Ala Trp Ile Phe Leu Ala Met
 25 30 35
 gct gct ggg ttg tta atc ggc aag gtc ttt cca gga att ggg gcg ctt 259
 Ala Ala Gly Leu Leu Ile Gly Lys Val Phe Pro Gly Ile Gly Ala Leu
 40 45 50
 ttg agc gcg gtg gaa att ggt gga att tcc att cca att gct atc ggt 307
 Leu Ser Ala Val Glu Ile Gly Gly Ile Ser Ile Pro Ile Ala Ile Gly
 55 60 65
 ttg atc gtc atg atg tat cca cct ttg gcc aag gtg cgc tac gac aaa 355
 Leu Ile Val Met Met Tyr Pro Pro Leu Ala Lys Val Arg Tyr Asp Lys
 70 75 80 85
 act aaa gaa atc agc aca gac cgc gct ctc atg gtg gtg tcg att atg 403
 Thr Lys Glu Ile Ser Thr Asp Arg Ala Leu Met Val Val Ser Ile Met
 90 95 100
 ttg aac tgg atc gtt gga cca gca ctt atg ttt agc ctg gcg tgg ctg 451

002290.80250960

[illegible]

345 350 355
 atc ttt aaa aag gag aat gca gga tca tgaatcagt ttgtttgtg 1218
 ile phe lys lys glu asn ala gly ser
 360 365
 tgc 1221

 <210> 120
 <211> 366
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 120
 Met ile glu gly trp leu met thr leu thr lys glu his ser thr pro
 1 5 10 15
 arg ala ala gly ser met ser phe leu asp arg trp leu ala ala trp
 20 25 30
 ile phe leu ala met ala ala gly leu leu ile gly lys val phe pro
 35 40 45
 gly ile gly ala leu leu ser ala val glu ile gly gly ile ser ile
 50 55 60
 pro ile ala ile gly leu leu val met met tyr pro pro leu ala lys
 65 70 75 80
 val arg tyr asp lys thr lys glu ile ser thr asp arg ala leu met
 85 90 95
 val val ser ile met leu asn trp ile val gly pro ala leu met phe
 100 105 110
 ser leu ala trp leu phe leu pro asp gln pro glu leu arg thr gly
 115 120 125
 leu ile ile val gly leu ala arg cys ile ala met val leu val trp
 130 135 140
 ser asp leu ala cys gly asp arg glu ala thr ala val leu val ala
 145 150 155 160
 ile asn ser val phe gln ile leu met phe gly val leu gly trp phe
 165 170 175
 tyr leu gln ile leu pro ser trp leu gly leu asp thr thr ser val
 180 185 190
 thr phe ser val val ser ile val thr ser val leu val phe leu gly
 195 200 205
 ile pro leu val ala gly val leu ser arg val ile gly glu lys thr
 210 215 220
 lys gly arg arg trp tyr glu asp thr phe leu pro lys ile ser pro
 225 230 235 240
 leu ala leu ile gly leu leu tyr thr ile val leu leu phe ser leu

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245 250 255

Gln Gly Asp Glu Ile Thr Ala Gln Pro Trp Thr Val Ala Arg Leu Ala
260 265 270

Leu Pro Leu Leu Met Tyr Phe Val Gly Met Phe Phe Ile Ser Leu Val
275 280 285

Val Ser Lys Leu Ser Gly Leu Thr Tyr Glu Arg Ala Ala Ser Val Ser
290 295 300

Phe Thr Ala Ala Gly Asn Phe Glu Leu Ala Ile Ala Val Ser Ile
305 310 315 320

Gly Thr Phe Gly Ala Thr Ser Pro Gln Ala Leu Ala Gly Thr Ile Gly
325 330 335

Pro Leu Ile Glu Val Pro Val Leu Val Gly Leu Val Tyr Val Met Leu
340 345 350

Trp Leu Gly Pro Lys Ile Phe Lys Lys Glu Asn Ala Gly Ser
355 360 365

<210> 121
<211> 1233
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1210)
<223> RXA02200

<400> 121
atttgtgtgga gagtgtgcat aaatccacta tatattgacg aatgtcgata ttgaaagtat 60
tttgaatatc gacaggtatc aatataccga aaggtgtcgc atg aca aac tca act 115
Met Thr Asn Ser Thr
1 5

cag acg cgg gcc aag cca gcc cga atc tca ttt ctt gat aaa tac att 163
Gln Thr Arg Ala Lys Pro Ala Arg Ile Ser Phe Leu Asp Lys Tyr Ile
10 15 20

cca ctt tgg att att ttg gcg atg gcg ttt ggg cta ttt tta ggc cgg 211
Pro Leu Trp Ile Ile Leu Ala Met Ala Phe Gly Leu Phe Leu Gly Arg
25 30 35

agc gtt tcg gga ctc tca ggc ttt cta ggc gca atg gaa gtc gga ggg 259
Ser Val Ser Gly Leu Ser Gly Phe Leu Gly Ala Met Glu Val Gly Gly
40 45 50

atc tcc ttg cca atc gct tta ggc ctc ctt gta atg atg tac cca ccg 307
Ile Ser Leu Pro Ile Ala Leu Gly Leu Leu Val Met Met Tyr Pro Pro
55 60 65

ttg gcc aaa gtt cgg tat gac aaa act aaa caa att gcc act gat aag 355
Leu Ala Lys Val Arg Tyr Asp Lys Thr Lys Gln Ile Ala Thr Asp Lys
70 75 80 85

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tta Leu	atg Met	ttc Phe	gcg Ala 105	cta Leu	gct Ala	tgg Trp	ttg Leu	ttc Phe 110	ctc Leu	cca Pro	gac Asp	caa Gln	ccg Pro 115	gaa Glu	tta Leu	451
cga Arg	acc Thr	ggc Gly 120	ctg Leu	att Ile	att Ile	gta Val	gga Gly 125	ctc Leu	gca Ala	cga Arg	tgt Cys	att Ile 130	gcg Ala	atg Met	gtc Val	499
ttg Leu	gtt Val	tgg Trp	tct Ser	gat Asp	atg Met	tcc Ser 140	tgt Cys	gga Gly	gac Asp	cgc Arg	gag Glu 145	gct Ala	aca Thr	gca Ala	gtt Val	547
ctc Leu 150	gta Val	gcc Ala	att Ile	aat Asn	tca Ser 155	gtt Val	ttt Phe	caa Gln	gtc Val	gca Ala 160	atg Met	ttt Phe	ggg Gly	gca Ala 165	ctt Leu	595
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acc Thr	acc Thr	gct Ala	caa Gln 185	ttc Phe	tct Ser	ttc Phe	tgg Trp	tca Ser 190	att Ile	gtg Val	act Thr	tcg Ser 195	gtt Val	ttg Leu	gtg Val	691
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gaa Glu 215	aag Lys	atc Ile	aag Lys	gga Gly	cgt Arg	gag Trp 220	tgg Trp	tat Tyr	gaa Glu	caa Gln	aag Lys 225	ttc Phe	ctt Leu	ccg Pro	gca Ala	787
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cggt Arg	ctc Leu	gcg Ala	ata Ile 265	cca Pro	ttg Leu	gtt Val	atc Ile	tat Tyr 270	ttc Phe	gtt Val	gga Gly	atg Met	ttt Phe 275	ttc Phe	att Ile	931
tca Ser	ctc Leu	att Ile 280	gcg Ala	tca Ser	aaa Lys	cta Leu	tct Ser 285	ggc Gly	atg Met	aac Asn	tat Tyr	gca Ala 290	aag Lys	tct Ser	gca Ala	979
tcc Ser	gtc Val	tct Ser	ttc Phe	act Thr	gca Ala	gct Ala 300	ggc Gly	aac Asn	aat Asn	ttt Phe	gaa Glu 305	ctt Leu	gcg Ala	att Ile	gcg Ala	1027
gtg Val 310	tcg Ser	atc Ile	gga Gly	acg Thr	ttt Phe 315	ggc Gly	gca Ala	act Thr	tct Ser	gca Ala 320	cag Gln	gct Val	atg Met	gca Ala	gga Gly 325	1075
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Lys Phe Leu Pro Ala Ile Ser Pro Phe Ala Leu Ile Gly Leu Leu Tyr
225 230 235 240

Thr Ile Val Leu Leu Phe Ser Leu Gln Gly Asp Gln Ile Val Ser Gln
245 250 255

Pro Trp Ala Val Val Arg Leu Ala Ile Pro Leu Val Ile Tyr Phe Val
260 265 270

Gly Met Phe Phe Ile Ser Leu Ile Ala Ser Lys Leu Ser Gly Met Asn
275 280 285

Tyr Ala Lys Ser Ala Ser Val Ser Phe Thr Ala Ala Gly Asn Asn Phe
290 295 300

Glu Leu Ala Ile Ala Val Ser Ile Gly Thr Phe Gly Ala Thr Ser Ala
305 310 315 320

Gln Ala Met Ala Gly Thr Ile Gly Pro Leu Ile Glu Ile Pro Val Leu
325 330 335

Val Gly Leu Val Tyr Ala Met Leu Trp Leu Gly Pro Lys Leu Phe Pro
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Asn Asp Pro Thr Leu Pro Ser Ser Ala Arg Ser Thr Ser Gln Ile Ile
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Asn Ser
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<223> RXA02202
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Met Thr Gly Gln Ala
1 5

gca cca aac ttg cat acc aat att ttg aac cgt atc gca aat gaa ctg 163
Ala Pro Asn Leu His Thr Asn Ile Leu Asn Arg Ile Ala Asn Glu Leu
10 15 20

gcg ttg acc tat caa gga gtt ttc tct gca gag act atc aac cgc tat 211
Ala Leu Thr Tyr Gln Gly Val Phe Ser Ala Glu Thr Ile Asn Arg Tyr
25 30 35

att ttt gaa tcg tat gtg tcg ttg gcg aga aca gca aaa atc cat acg 259
Ile Phe Glu Ser Tyr Val Ser Leu Ala Arg Thr Ala Lys Ile His Thr
40 45 50

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 His Leu Pro Ile Leu Ala Glu Gly Phe Ala Lys Asp Arg Leu His Ala
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 ctt gcg gta gct gaa ggt aag gtg gct tca cct gtg cct cag gtc cta 355
 Leu Ala Val Ala Glu Gly Lys Val Ala Ser Pro Val Pro Gln Val Leu
 70 75 80 85
 ttt att tgc gtc cac aac gca ggt cgt tca caa att gct tgc gcg ttg 403
 Phe Ile Cys Val His Asn Ala Gly Arg Ser Gln Ile Ala Ser Ala Leu
 90 95 100
 ttg tct cac tat gcc ggt agt tct gta gag gta cgt tct gca ggt tct 451
 Leu Ser His Tyr Ala Gly Ser Ser Val Glu Val Arg Ser Ala Gly Ser
 105 110 115
 tta cct gct tct gaa att cac cca ctg gtg ttg gaa att ttg tca gag 499
 Leu Pro Ala Ser Glu Ile His Pro Leu Val Leu Glu Ile Leu Ser Glu
 120 125 130
 cga gga gtg aac att tct gat gca ttt ccg aaa ccg cta acc gat gat 547
 Arg Gly Val Asn Ile Ser Asp Ala Phe Pro Lys Pro Leu Thr Asp Asp
 135 140 145
 gtt att cgc gca tct gac tat gtc ata aca atg gga tgt gga gat gtg 595
 Val Ile Arg Ala Ser Asp Tyr Val Ile Thr Met Gly Cys Gly Asp Val
 150 155 160 165
 tgc cca atg tat cca gga aag cac tat ctc gat tgg gag ctc gct gat 643
 Cys Pro Met Tyr Pro Gly Lys His Tyr Leu Asp Trp Glu Leu Ala Asp
 170 175 180
 ccg tca gat gaa ggt gag gac aag ata cag gaa ata att gag gaa att 691
 Pro Ser Asp Glu Gly Glu Asp Lys Ile Gln Glu Ile Ile Glu Glu Ile
 185 190 195
 gac ggt cga atc cgc gag ctt tgg aaa agc att caa tta tgc caa aac 739
 Asp Gly Arg Ile Arg Glu Leu Trp Lys Ser Ile Gln Leu Ser Gln Asn
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 taggcagtca aaggtctggc acc 762

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 Thr Ile Asn Arg Tyr Ile Phe Glu Ser Tyr Val Ser Leu Ala Arg Thr
 35 40 45
 Ala Lys Ile His Thr His Leu Pro Ile Leu Ala Glu Gly Phe Ala Lys
 50 55 60

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Asp Arg Leu His Ala Leu Ala Val Ala Glu Gly Lys Val Ala Ser Pro
65 70 75 80

Val Pro Gln Val Leu Phe Ile Cys Val His Asn Ala Gly Arg Ser Gln
85 90 95

Ile Ala Ser Ala Leu Leu Ser His Tyr Ala Gly Ser Ser Val Glu Val
100 105 110

Arg Ser Ala Gly Ser Leu Pro Ala Ser Glu Ile His Pro Leu Val Leu
115 120 125

Glu Ile Leu Ser Glu Arg Gly Val Asn Ile Ser Asp Ala Phe Pro Lys
130 135 140

Pro Leu Thr Asp Asp Val Ile Arg Ala Ser Asp Tyr Val Ile Thr Met
145 150 155 160

Gly Cys Gly Asp Val Cys Pro Met Tyr Pro Gly Lys His Tyr Leu Asp
165 170 175

Trp Glu Leu Ala Asp Pro Ser Asp Glu Gly Glu Asp Lys Ile Gln Glu
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Gln Leu Ser Gln Asn
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Val Asn Glu Glu Ile
1 5

acc ctc cta gcc gca gca gca gat cct gcc gca act gaa aat att ggc 163
Thr Leu Leu Ala Ala Ala Ala Asp Pro Ala Ala Thr Glu Asn Ile Gly
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tgg gta caa acc att gtg ctc tcc atc gtt caa ggc ctc aca gag ttc 211
Trp Val Gln Thr Ile Val Leu Ser Ile Val Gln Gly Leu Thr Glu Phe
25 30 35

ctg ccg atc agc tcc agc gga cac ctc cga atc atc tct gag ctg ttc 259
Leu Pro Ile Ser Ser Ser Gly His Leu Arg Ile Ile Ser Glu Leu Phe
40 45 50

tgg ggt gcc gat gcc ggc gcg tcc ttt acc gcc gtg gtt cag ctt ggt 307

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Trp Gly Ala Asp Ala Gly Ala Ser Phe Thr Ala Val Val Gln Leu Gly
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 acc gaa gcc gca gtg ctg gtg ttt ttt gcc aag gaa atc tgg caa atc 355
 Thr Glu Ala Ala Val Leu Val Phe Phe Ala Lys Glu Ile Trp Gln Ile
 70 75 80 85
 atc aca ggt tgg ttc gct ggc gta ttc aat aag gaa cgc cgc gga ttt 403
 Ile Thr Gly Trp Phe Ala Gly Val Phe Asn Lys Glu Arg Arg Gly Phe
 90 95 100
 gaa tac cgc atg ggc tgg atg atc att gtt gcc acc att ccc gtc gtg 451
 Glu Tyr Arg Met Gly Trp Met Ile Ile Val Ala Thr Ile Pro Val Val
 105 110 115
 atc ttg ggt gtg ttg ggc aag gac ctg atc cgt gag gcg ctg cga aat 499
 Ile Leu Gly Val Leu Gly Lys Asp Leu Ile Arg Glu Ala Leu Arg Asn
 120 125 130
 atg tgg atc act gca tcc gtg ctg atc ctg ttc tcc ctg gtg ttc att 547
 Met Trp Ile Thr Ala Ser Val Leu Ile Leu Phe Ser Leu Val Phe Ile
 135 140 145
 ttg gcc gag aag atg ggc aag aag gaa cgc gac tac gac aaa ctg acc 595
 Leu Ala Glu Lys Met Gly Lys Lys Glu Arg Asp Tyr Asp Lys Leu Thr
 150 155 160 165
 atg aaa gat gcc atc atc atg ggt ctt gca cag tgt ctt gcg ctg atc 643
 Met Lys Asp Ala Ile Ile Met Gly Leu Ala Gln Cys Leu Ala Leu Ile
 170 175 180
 cct ggc gtg tct cgc tcc ggc ggc acc atc tct gct ggt ttg ttc ctt 691
 Pro Gly Val Ser Arg Ser Gly Gly Thr Ile Ser Ala Gly Leu Phe Leu
 185 190 195
 ggt ctc aag cgt gaa gta gcc acc aag ttc tcc ttc ctg ctg gca atc 739
 Gly Leu Lys Arg Glu Val Ala Thr Lys Phe Ser Phe Leu Ala Ile
 200 205 210
 cct gca gtg ctt ggc tcc ggt ttg tac tcc ctg cct gac gct ttt gcg 787
 Pro Ala Val Leu Gly Ser Gly Leu Tyr Ser Leu Pro Asp Ala Phe Ala
 215 220 225
 cca agc tcc gga caa gct gcc tcc ggc cta cag ctc acc gtg ggt acc 835
 Pro Ser Ser Gly Gln Ala Ala Ser Gly Leu Gln Leu Thr Val Gly Thr
 230 235 240 245
 ctg gtt gcc ttc gta gtt ggc tac att tcc att gcg tgg ctg atg aag 883
 Leu Val Ala Phe Val Val Gly Tyr Ile Ser Ile Ala Trp Leu Met Lys
 250 255 260
 ttc gtg gca aac cac tcc ttc agc tgg ttt gct gca tac cgt att cct 931
 Phe Val Ala Asn His Ser Phe Ser Trp Phe Ala Ala Tyr Arg Ile Pro
 265 270 275
 gca ggt ctg ctc gtg atg ctg ctg ctc gca ctg ggc atg ctc aac cca 979
 Ala Gly Leu Leu Val Met Leu Leu Leu Ala Leu Gly Met Leu Asn Pro
 280 285 290
 taaaattcct gtacatctta aaa 1002

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0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

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Gly	Leu	Thr	Glu	Phe	Leu	Pro	Ile	Ser	Ser	Ser	Gly	His	Leu	Arg	Ile	
		35					40					45				
Ile	Ser	Glu	Leu	Phe	Trp	Gly	Ala	Asp	Ala	Gly	Ala	Ser	Phe	Thr	Ala	
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Val	Val	Gln	Leu	Gly	Thr	Glu	Ala	Ala	Val	Leu	Val	Phe	Phe	Ala	Lys	
	65				70					75					80	
Glu	Ile	Trp	Gln	Ile	Ile	Thr	Gly	Trp	Phe	Ala	Gly	Val	Phe	Asn	Lys	
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Glu	Arg	Arg	Gly	Phe	Glu	Tyr	Arg	Met	Gly	Trp	Met	Ile	Ile	Val	Ala	
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Thr	Ile	Pro	Val	Val	Ile	Leu	Gly	Val	Leu	Gly	Lys	Asp	Leu	Ile	Arg	
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Glu	Ala	Leu	Arg	Asn	Met	Trp	Ile	Thr	Ala	Ser	Val	Leu	Ile	Leu	Phe	
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Ser	Leu	Val	Phe	Ile	Leu	Ala	Glu	Lys	Met	Gly	Lys	Lys	Glu	Arg	Asp	
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Tyr	Asp	Lys	Leu	Thr	Met	Lys	Asp	Ala	Ile	Ile	Met	Gly	Leu	Ala	Gln	
				165					170					175		
Cys	Leu	Ala	Leu	Ile	Pro	Gly	Val	Ser	Arg	Ser	Gly	Gly	Thr	Ile	Ser	
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Ala	Gly	Leu	Phe	Leu	Gly	Leu	Lys	Arg	Glu	Val	Ala	Thr	Lys	Phe	Ser	
	195						200					205				
Phe	Leu	Leu	Ala	Ile	Pro	Ala	Val	Leu	Gly	Ser	Gly	Leu	Tyr	Ser	Leu	
	210					215					220					
Pro	Asp	Ala	Phe	Ala	Pro	Ser	Ser	Gly	Gln	Ala	Ala	Ser	Gly	Leu	Gln	
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Leu	Thr	Val	Gly	Thr	Leu	Val	Ala	Phe	Val	Val	Gly	Tyr	Ile	Ser	Ile	
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Ala	Trp	Leu	Met	Lys	Phe	Val	Ala	Asn	His	Ser	Phe	Ser	Trp	Phe	Ala	
			260					265					270			
Ala	Tyr	Arg	Ile	Pro	Ala	Gly	Leu	Leu	Val	Met	Leu	Leu	Leu	Ala	Leu	
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Val Arg Gly Ile Ala
1 5
cgc gcg atc gtg cca gac ctt gaa cgc gga caa aag gct gcg cac gcc 163
Arg Ala Ile Val Pro Asp Leu Glu Arg Gly Gln Lys Ala Ala His Ala
10 15 20
ttt gca ctg ctg atg att att cag gga att gct ccc gtg gta gct ccg 211
Phe Ala Leu Leu Met Ile Ile Gln Gly Ile Ala Pro Val Val Ala Pro
25 30 35
ctc att ggt ggt gtg ctg gtc ggg cct ttt ggc tgg cgg gga att ttc 259
Leu Ile Gly Gly Val Leu Val Gly Pro Phe Gly Trp Arg Gly Ile Phe
40 45 50
tgg gca ctt gca ctg gtg aat ttt gcg cag ctg ctt gtt gct ttg ctg 307
Trp Ala Leu Ala Leu Val Asn Phe Ala Gln Leu Leu Val Ala Leu Leu
55 60 65
cag att aag gag tcg aag cca gtt gaa gag cgt acc gca gca gga ctt 355
Gln Ile Lys Glu Ser Lys Pro Val Glu Glu Arg Thr Ala Ala Gly Leu
70 75 80 85
ggc gga atg ctg tcc aac tat gtc ttt gtg ctg aag aat cct caa ttt 403
Gly Gly Met Leu Ser Asn Tyr Val Phe Val Leu Lys Asn Pro Gln Phe
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Leu Ala Tyr Val Phe Thr Leu Gly Leu Ser Phe Gly Ala Met Phe Ser
105 110 115
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Tyr Ile Ser Ala Ser Pro Phe Val Leu Gln Asn Gln Met Gly Ile Pro
120 125 130
gta ctg ctg tat tcc att att ttc gga gtg aat gct ttt ggt ttg att 547
Val Leu Leu Tyr Ser Ile Ile Phe Gly Val Asn Ala Phe Gly Leu Ile
135 140 145
gtg ggc gga atg gtc aat agg cga ctt ctg cag cgg att cat cca cac 595
Val Gly Gly Met Val Asn Arg Arg Leu Leu Arg Ile His Pro His
150 155 160 165

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ttg ctg att gaa gtg ctg ttt att aat tgg ata ccg ctg ttc ctg ttg 691
 Leu Leu Ile Glu Val Leu Phe Ile Asn Trp Ile Pro Leu Phe Leu Leu
 185 190 195

ctg ctg ttt ctt atc gtt tcc cat att cgg atg gtt atg gct aac gcg 739
 Leu Leu Phe Leu Ile Val Ser His Ile Pro Met Val Met Ala Asn Ala
 200 205 210

aca gct ctg gga act gaa gtg gtg cga agc agg gcg gga tcg ggt tct 787
 Thr Ala Leu Gly Thr Glu Val Val Arg Ser Arg Ala Gly Ser Gly Ser
 215 220 225

gca att ttg ggt ttc gtg caa ttc acg atg ggt gct ttg gtg agt tca 835
 Ala Ile Leu Gly Phe Val Gln Phe Thr Met Gly Ala Leu Val Ser Ser
 230 235 240 245

ctg gtc gga tta ggc tct gat aag gct ttg act atg gga atc gca atg 883
 Leu Val Gly Leu Gly Ser Asp Lys Ala Leu Thr Met Gly Ile Ala Met
 250 255 260

act gct tgt gca ctg ctg gcg tgt ggg tgt gcg tac ctg gca ggt cga 931
 Thr Ala Cys Ala Leu Leu Ala Cys Gly Cys Ala Tyr Leu Ala Gly Arg
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 Lys Gly Ile Pro Glu Met Lys
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<210> 128
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 128
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Lys Ala Ala His Ala Phe Ala Leu Leu Met Ile Ile Gln Gly Ile Ala
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 35 40 45

Trp Arg Gly Ile Phe Trp Ala Leu Ala Leu Val Asn Phe Ala Gln Leu
 50 55 60

Leu Val Ala Leu Leu Gln Ile Lys Glu Ser Lys Pro Val Glu Glu Arg
 65 70 75 80

Thr Ala Ala Gly Leu Gly Gly Met Leu Ser Asn Tyr Val Phe Val Leu
 85 90 95

Lys Asn Pro Gln Phe Leu Ala Tyr Val Phe Thr Leu Gly Leu Ser Phe
 100 105 110

Gly Ala Met Phe Ser Tyr Ile Ser Ala Ser Pro Phe Val Leu Gln Asn

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115 120 125

Gln Met Gly Ile Pro Val Leu Leu Tyr Ser Ile Ile Phe Gly Val Asn
130 135 140

Ala Phe Gly Leu Ile Val Gly Gly Met Val Asn Arg Arg Leu Leu Gln
145 150 155 160

Arg Ile His Pro His Arg Ile Met Gln Thr Val Leu Ala Ser Phe Thr
165 170 175

Val Leu Cys Ala Leu Leu Leu Ile Glu Val Leu Phe Ile Asn Trp Ile
180 185 190

Pro Leu Phe Leu Leu Leu Leu Phe Leu Ile Val Ser His Ile Pro Met
195 200 205

Val Met Ala Asn Ala Thr Ala Leu Gly Thr Glu Val Val Arg Ser Arg
210 215 220

Ala Gly Ser Gly Ser Ala Ile Leu Gly Phe Val Gln Phe Thr Met Gly
225 230 235 240

Ala Leu Val Ser Ser Leu Val Gly Leu Gly Ser Asp Lys Ala Leu Thr
245 250 255

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260 265 270

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<213> Corynebacterium glutamicum

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<223> RXN00901

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Met Gln Lys Lys Gln
1 5

cag ctg agc acc gcc ctg att atg gga ttg gca tta ttg tca gcc agc 163
Gln Leu Ser Thr Ala Leu Ile Met Gly Leu Ala Leu Leu Ser Ala Ser
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tcc gcg cta gcg act gat atg tat ttg ccg gca atg cct ggt att gcg 211
Ser Ala Leu Ala Thr Asp Met Tyr Leu Pro Ala Met Pro Gly Ile Ala
25 30 35

gaa gat ttg ggg aca act gca ccg atg gtg cag tta act ctt tct tcc 259
Glu Asp Leu Gly Thr Thr Ala Pro Met Val Gln Leu Thr Leu Ser Ser
40 45 50

00603200.062300

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Phe	Met	Ala	Gly	Met	Ala	Ile	Gly	Gln	Leu	Ile	Ile	Gly	Pro	Leu	Ser	
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Asp	Gln	Leu	Gly	Arg	Lys	Gly	Leu	Leu	Val	Ala	Gly	Ala	Val	Ala	Ala	
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ctg	gtc	gct	agt	gtg	gtg	tgc	gcg	ctg	gcg	ccg	tcg	ata	agc	gta	tta	403
Leu	Val	Ala	Ser	Val	Val	Cys	Ala	Leu	Ala	Pro	Ser	Ile	Ser	Val	Leu	
				90					95					100		
gtg	atc	gca	cgc	ctg	gtg	cag	ggg	ctt	ggc	ggc	ggt	gcg	tgc	gtg	gta	451
Val	Ile	Ala	Arg	Leu	Val	Gln	Gly	Leu	Gly	Gly	Gly	Ala	Cys	Val	Val	
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Leu	Arg	Ala	Arg	Ser	Cys	Gln	Thr	Leu	Asn	Ala	Asp	Lys	Arg	Leu	Arg	
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<213> Corynebacterium glutamicum																
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Met	Pro	Gly	Ile	Ala	Glu	Asp	Leu	Gly	Thr	Thr	Ala	Pro	Met	Val	Gln	
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Leu	Thr	Leu	Ser	Ser	Phe	Met	Ala	Gly	Met	Ala	Ile	Gly	Gln	Leu	Ile	
	50				55						60					
Ile	Gly	Pro	Leu	Ser	Asp	Gln	Leu	Gly	Arg	Lys	Gly	Leu	Leu	Val	Ala	
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Gly	Ala	Val	Ala	Ala	Leu	Val	Ala	Ser	Val	Val	Cys	Ala	Leu	Ala	Pro	
			85						90					95		
Ser	Ile	Ser	Val	Leu	Val	Ile	Ala	Arg	Leu	Val	Gln	Gly	Leu	Gly	Gly	
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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 Met Gly Leu Ala Leu
 1 5
 t t g t c a g c c a g c t c c g c g c t a g c g a c t g a t a t g t a t t t g c c g g c a a t g 163
 Leu Ser Ala Ser Ser Ala Leu Ala Thr Asp Met Tyr Leu Pro Ala Met
 10 15 20
 c c t g g t a t t g c g g a a g a t t t g g g a c a a c t g c a c c g a t g t g c a g t t a 211
 Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala Pro Met Val Gln Leu
 25 30 35
 a c t c t t t c t c c t t t a t g g c t g g a a t g g c g a t t g g c c a a t t g a t c a t t 259
 Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile Gly Gln Leu Ile Ile
 40 45 50
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 Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly Leu Leu Val Ala Gly
 55 60 65
 g c g g t g c t g c g c t g c g c t a g t g t g t g c g c g c t g c g c c g t c g 355
 Ala Val Ala Ala Leu Val Ala Ser Val Val Cys Ala Leu Ala Pro Ser
 70 75 80 85
 a t a a g c g t a t t a g t g a t c g c a c g c t g t g c a g g g c t t g g c g g c g g t 403
 Ile Ser Val Leu Val Ile Ala Arg Leu Val Gln Gly Leu Gly Gly Gly
 90 95 100
 g c g t g c g t g t a t t g c g c g c g a t c g t g c a g a c c t t g a a c g c g g a c 451
 Ala Cys Val Val Leu Arg Ala Arg Ser Cys Gln Thr Leu Asn Ala Asp
 105 110 115
 a a a a g g c t g c g c a c g c c t t t g c a c t g c t g a t g a t t a t t c a g g g a a t t 498
 Lys Arg Leu Arg Thr Pro Leu His Cys
 120 125
 g c t 501

<210> 132
 <211> 126
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 132
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 Tyr Leu Pro Ala Met Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala

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Pro Met Val Gln Leu Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile		
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Gly Gln Leu Ile Ile Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly		
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Leu Leu Val Ala Gly Ala Val Ala Ala Leu Val Ala Ser Val Val Cys		
65	70	75
Ala Leu Ala Pro Ser Ile Ser Val Leu Val Ile Ala Arg Leu Val Gln		
85	90	95
Gly Leu Gly Gly Gly Ala Cys Val Val Leu Arg Ala Arg Ser Cys Gln		
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1276)
 <223> RXA00289

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 Met Ser Thr Thr Thr
 1 5
 gcg ccc gaa gca cgg ttt cct gtc gtc cct ttg acc gcc atg agt ttc 163
 Ala Pro Glu Ala Arg Phe Pro Val Val Pro Leu Thr Ala Met Ser Phe
 10 15 20
 gcg gca ttt gtt tat gtc acg ttc gag atg ttt gca gtt gcc ctg atc 211
 Ala Ala Phe Val Tyr Val Thr Phe Glu Met Phe Ala Val Gly Leu Ile
 25 30 35
 aag ccg atg gcc agc gat ctt gga gtg tca gaa tcc agc atc gcc ctg 259
 Lys Pro Met Ala Ser Asp Leu Gly Val Ser Glu Ser Ser Ile Gly Leu
 40 45 50
 ttg atg act gtg tat gcg act gtc gtt gcc gtg gtg acg atc cct gcc 307
 Leu Met Thr Val Tyr Ala Thr Val Val Ala Val Val Thr Ile Pro Ala
 55 60 65
 atg ttg tgg gtt tct cga ttt aac aag cgc aca gtt ttc ctg att act 355
 Met Leu Trp Val Ser Arg Phe Asn Lys Arg Thr Val Phe Leu Ile Thr
 70 75 80 85
 ctg gca ttt ttg gcc acg gcc att gtt gtt cag gca ctg acc gtt aat 403
 Leu Ala Phe Leu Ala Thr Gly Ile Val Val Gln Ala Leu Thr Val Asn
 90 95 100

00230-802E0960

tat gga atg cta gcc atc ggc cgc act atc gca gca ttg act cac ggg 451
 Tyr Gly Met Leu Ala Ile Gly Arg Thr Ile Ala Ala Leu Thr His Gly
 105 110 115

gtg ttt tgg gca ctt gtt ggg cca atg gca gcg cgt atg tcc cca ggt 499
 Val Phe Trp Ala Leu Val Gly Pro Met Ala Ala Arg Met Ser Pro Gly
 120 125 130

cac act ggt cgt gca gta ggc gtt gtg tgc att gga tca acc atg gcg 547
 His Thr Gly Arg Ala Val Gly Val Val Ser Ile Gly Ser Thr Met Ala
 135 140 145

ctg gtc gtt ggt tct ccg ctg gca aca tgg atc ggt gaa ctc atc gga 595
 Leu Val Val Gly Ser Pro Leu Ala Thr Trp Ile Gly Glu Leu Ile Gly
 150 155 160 165

tgg cgt cct gcc acc tgg att ctt ggt gcg ctg acc att gcg gcc gtg 643
 Trp Arg Pro Ala Thr Trp Ile Leu Gly Ala Leu Thr Ile Ala Ala Val
 170 175 180

gct gta ctc att cca acc gtt cca tca ctg cca cca ctt cca gac acg 691
 Ala Val Leu Ile Pro Thr Val Pro Ser Leu Pro Pro Leu Pro Asp Thr
 185 190 195

gaa tca gag tcc aaa gaa aag aaa tcc ctt cca tgg ggt ctc att tcc 739
 Glu Ser Glu Ser Lys Glu Lys Lys Ser Leu Pro Trp Gly Leu Ile Ser
 200 205 210

ctg gtc att ttc ctt ctc ctt gcc gtc acc ggt gtt ttt gct gcc tac 787
 Leu Val Ile Phe Leu Leu Leu Ala Val Thr Gly Val Phe Ala Ala Tyr
 215 220 225

acc tac ctt gcc ctc atc atc gct gaa aca gca ggg gac agc ttc gtg 835
 Thr Tyr Leu Gly Leu Ile Ile Ala Glu Thr Ala Gly Asp Ser Phe Val
 230 235 240 245

tcc att gcc ttg ttc gcc ttc ggt gca ctc gga ctc att gcc gtg aca 883
 Ser Ile Gly Leu Phe Ala Phe Gly Ala Leu Gly Leu Ile Gly Val Thr
 250 255 260

gtg gca acc cga act gtg gat caa gcg atg ctg cgt gga agt gtt cac 931
 Val Ala Thr Arg Thr Val Asp Gln Arg Met Leu Arg Gly Ser Val His
 265 270 275

acc acc act ttg ttt gtc att gct gca att ctc gga cag atc gca ttc 979
 Thr Thr Thr Leu Phe Val Ile Ala Ala Ile Leu Gly Gln Ile Ala Phe
 280 285 290

gga tta gag ggc aca cta gcc gta gta gct atc ttc ctt gca gtc acc 1027
 Gly Leu Glu Gly Thr Leu Ala Val Val Ala Ile Phe Leu Ala Val Thr
 295 300 305

gtg ttt ggt gga gca tac ggc gct ctc cca acc ctg gga acc acc atc 1075
 Val Phe Gly Gly Ala Tyr Gly Ala Leu Pro Thr Thr Thr Thr Ile
 310 315 320 325

ttc ctc cat gcg ggt cgc gac cac cca gat act gca tcc tcc att tat 1123
 Phe Leu His Ala Gly Arg Asp His Pro Asp Thr Ala Ser Ser Ile Tyr
 330 335 340

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gtg gtc act tac caa gtg ggt atc gcg tct ggc gcg gca ctt ggc gcg 1171
 Val Val Thr Tyr Gln Val Gly Ile Ala Ser Gly Ala Ala Leu Gly Ala
 345 350 355

atg gct gtg gat gcc gat tgg gtt gct ggc act ttg tgg atc atg gct 1219
 Met Ala Val Asp Ala Asp Trp Val Ala Gly Thr Leu Trp Ile Met Ala
 360 365 370

gga ctg tca ttg gct tcc acg ttg gcc ttg gcg ctg tgg tcc cgc ccg 1267
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 375 380 385

cta ctg aag tagcagccca aattcagcc act 1299
 Leu Leu Lys
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<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

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Thr Ala Met Ser Phe Ala Ala Phe Val Tyr Val Thr Phe Glu Met Phe
 20 25 30

Ala Val Gly Leu Ile Lys Pro Met Ala Ser Asp Leu Gly Val Ser Glu
 35 40 45

Ser Ser Ile Gly Leu Leu Met Thr Val Tyr Ala Thr Val Val Ala Val
 50 55 60

Val Thr Ile Pro Ala Met Leu Trp Val Ser Arg Phe Asn Lys Arg Thr
 65 70 75 80

Val Phe Leu Ile Thr Leu Ala Phe Leu Ala Thr Gly Ile Val Val Gln
 85 90 95

Ala Leu Thr Val Asn Tyr Gly Met Leu Ala Ile Gly Arg Thr Ile Ala
 100 105 110

Ala Leu Thr His Gly Val Phe Trp Ala Leu Val Gly Pro Met Ala Ala
 115 120 125

Arg Met Ser Pro Gly His Thr Gly Arg Ala Val Gly Val Val Ser Ile
 130 135 140

Gly Ser Thr Met Ala Leu Val Val Gly Ser Pro Leu Ala Thr Trp Ile
 145 150 155 160

Gly Glu Leu Ile Gly Trp Arg Pro Ala Thr Trp Ile Leu Gly Ala Leu
 165 170 175

Thr Ile Ala Ala Val Ala Val Leu Ile Pro Thr Val Pro Ser Leu Pro
 180 185 190

Pro Leu Pro Asp Thr Glu Ser Glu Ser Lys Glu Lys Lys Ser Leu Pro
 195 200 205

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Trp Gly Leu Ile Ser Leu Val Ile Phe Leu Leu Leu Ala Val Thr Gly
 210 215 220
 Val Phe Ala Ala Tyr Thr Tyr Leu Gly Leu Ile Ile Ala Glu Thr Ala
 225 230 235 240
 Gly Asp Ser Phe Val Ser Ile Gly Leu Phe Ala Phe Gly Ala Leu Gly
 245 250 255
 Leu Ile Gly Val Thr Val Ala Thr Arg Thr Val Asp Gln Arg Met Leu
 260 265 270
 Arg Gly Ser Val His Thr Thr Thr Leu Phe Val Ile Ala Ala Ile Leu
 275 280 285
 Gly Gln Ile Ala Phe Gly Leu Glu Gly Thr Leu Ala Val Val Ala Ile
 290 295 300
 Phe Leu Ala Val Thr Val Phe Gly Gly Ala Tyr Gly Ala Leu Pro Thr
 305 310 315 320
 Leu Gly Thr Thr Ile Phe Leu His Ala Gly Arg Asp His Pro Asp Thr
 325 330 335
 Ala Ser Ser Ile Tyr Val Val Thr Tyr Gln Val Gly Ile Ala Ser Gly
 340 345 350
 Ala Ala Leu Gly Ala Met Ala Val Asp Ala Asp Trp Val Ala Gly Thr
 355 360 365
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 370 375 380
 Leu Trp Ser Arg Pro Leu Leu Lys
 385 390

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 <223> RXN01984

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 Met His Glu Ser Gly
 1 5
 aaa aat cct gtc aag gtt gtc gac tcg cag gca cca caa gga cgc ggt 163
 Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala Pro Gln Gly Arg Gly
 10 15 20
 ggg cat atc gcc gga cat atc aaa cgc cgc ccg att cct agg caa acg 211
 Gly His Ile Gly Gly His Ile Lys Arg Arg Pro Ile Pro Arg Gln Thr

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Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met Thr Ala Leu Ala Leu			
40	45	50	
ggt ggc ttc gcc atc ggt gtg acg gaa ttt gtc tcc atg ggt ctg ctc			307
Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val Ser Met Gly Leu Leu			
55	60	65	
agc gcg atc gcc tcc gac ttt gag atc tcc gaa gac caa gcc gga cac			355
Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu Asp Gln Ala Gly His			
70	75	80	85
atc atc acc atc tac gcc ctc gcg tgg ttg tgg gtg ccc cgc			397
Ile Ile Thr Ile Tyr Ala Leu Ala Trp Leu Trp Val Pro Arg			
90	95		
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<210> 136
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 136
 Met His Glu Ser Gly Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala
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 Ile Pro Arg Gln Thr Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met
 35 40 45
 Thr Ala Leu Ala Leu Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val
 50 55 60
 Ser Met Gly Leu Leu Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu
 65 70 75 80
 Asp Gln Ala Gly His Ile Ile Thr Ile Tyr Ala Leu Ala Trp Leu Trp
 85 90 95
 Val Pro Arg

<210> 137
 <211> 379
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(379)
 <223> FRXA01984

<400> 137
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caatagtgcc ggtgagggag ctgtccgata ttgtgcttac atg cac gaa tct gga 115
Met His Glu Ser Gly
1 5

aaa aat cct gtc aag gtt gtc gac tcg cag gca cca caa gga cgc ggt 163
Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala Pro Gln Gly Arg Gly
10 15 20

ggg cat atc ggc gga cat atc aaa cgc cgc ccg att oct agg caa acg 211
Gly His Ile Gly Gly His Ile Lys Arg Arg Pro Ile Pro Arg Gln Thr
25 30 35

gaa att tcc gag gtt cgt cga tat atc gtc atg act gcc ctc gca ctc 259
Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met Thr Ala Leu Ala Leu
40 45 50

ggt ggc ttc gcc atc ggt gtg acg gaa ttt gtc tcc atg ggt ctg ctc 307
Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val Ser Met Gly Leu Leu
55 60 65

agc gcg atc gcc tcc gac ttt gag atc tcc gaa gac caa gcc gga cac 355
 Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu Asp Gln Ala Gly His
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atc atc acc atc tac gcc ctc gcg 379
Ile Ile Thr Ile Tyr Ala Leu Ala
90

<210> 138

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 138

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20 25 30

Ile Pro Arg Gln Thr Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met
35 40 45

Thr Ala Leu Ala Leu Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val
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Ser Met Gly Leu Leu Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu
65 70 75 80

Asp Gln Ala Gly His Ile Ile Thr Ile Tyr Ala Leu Ala
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<210> 139

<211> 735

<212> DNA

<213> *Corynebacterium glutamicum*

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<223> RXA00109
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				Val	Ala	Ser	Glu	Lys	
					1			5	
aat cta aaa ttg cgt acc ttg gcg gca gct gct ggg gtg ttg ggc gtt	163								
Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Gly Val Leu Gly Val									
	10			15				20	
ggc gcg atg tgc atg ctc gtg gct ccg cag gct gct gcc cat gat gtg	211								
Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala Ala Ala His Asp Val									
	25			30				35	
gtg gtg gat tct aat cct gaa aat ggc agt gtc gtt gat gag ttc ccg	259								
Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val Val Asp Glu Phe Pro									
	40			45				50	
gag acc att gag ttg gag gtt tcc ggt att cct cag gat ctg ttc aca	307								
Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro Gln Asp Leu Phe Thr									
	55			60				65	
aca gtt gca ttg agc aat gcg gat tcc gga gag gtg tta act tct gga	355								
Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu Val Leu Thr Ser Gly									
	70			75				80	
act cct cag ctt gag ggg cag cac ttg agc tat gaa gtg cca tct gat	403								
Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr Glu Val Pro Ser Asp									
	90			95				100	
gtg cag acg gga gct ggt aac tac att ttg ggt ttc cag atc act tct	451								
Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly Phe Gln Ile Thr Ser									
	105			110				115	
tct gat ggt cac gct act aaa ggt tca atc tct ttt gag gtg aca ggc	499								
Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser Phe Glu Val Thr Gly									
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tct gct gaa acg aca aca gag aca aca gca gag acg aca act gag tca	547								
Ser Ala Glu Thr Thr Thr Glu Thr Thr Thr Ala Glu Thr Thr Glu Ser									
	135			140				145	
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Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu Ala Glu Thr Thr Glu									
	150			155				160	
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Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro Trp Asn Trp Val Leu									
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agc atc gtg gcg gtg ctt gtt gtt gca agt gcc atc gtc atg atg att	691								
Ser Ile Val Val Ala Val Leu Val Val Ala Ser Ala Ile Val Met Met Ile									
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gca aag aat cgt aac cag aaa taagagggtt tattccacat gaa	735								
Ala Lys Asn Arg Asn Gln Lys									

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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Ala Ala His Asp Val Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val
 35 40 45
 Val Asp Glu Phe Pro Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro
 50 55 60
 Gln Asp Leu Phe Thr Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu
 65 70 75 80
 Val Leu Thr Ser Gly Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr
 85 90 95
 Glu Val Pro Ser Asp Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly
 100 105 110
 Phe Gln Ile Thr Ser Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser
 115 120 125
 Phe Glu Val Thr Gly Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu
 130 135 140
 Thr Thr Thr Glu Ser Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu
 145 150 155 160
 Ala Glu Thr Thr Glu Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro
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 <223> RXA00109

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Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Ala Gly Val Leu Gly Val									
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Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala Ala Ala His Asp Val									
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Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val Val Asp Glu Phe Pro									
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Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro Gln Asp Leu Phe Thr									
	55			60				65	
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Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu Val Leu Thr Ser Gly									
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Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr Glu Val Pro Ser Asp									
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Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly Phe Gln Ile Thr Ser									
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Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser Phe Glu Val Thr Gly									
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Ser Ala Glu Thr Thr Thr Glu Thr Thr Thr Ala Glu Thr Thr Thr Glu Ser									
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Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Thr Glu Ala Glu Thr Thr Glu									
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Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro Trp Asn Trp Val Leu									
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Ser Ile Val Ala Val Leu Val Val Ala Ser Ala Ile Val Met Met Ile									
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<213> Corynebacterium glutamicum

<400> 142

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Val Asp Glu Phe Pro Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro
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Gln Asp Leu Phe Thr Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu
 65 70 75 80

Val Leu Thr Ser Gly Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr
 85 90 95

Glu Val Pro Ser Asp Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly
 100 105 110

Phe Gln Ile Thr Ser Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser
 115 120 125

Phe Glu Val Thr Gly Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu
 130 135 140

Thr Thr Thr Glu Ser Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu
 145 150 155 160

Ala Glu Thr Thr Glu Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro
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Trp Asn Trp Val Leu Ser Ile Val Ala Val Leu Val Val Ala Ser Ala
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Ile Val Met Met Ile Ala Lys Asn Arg Asn Gln Lys
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<220>

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<223> RXA00996

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 Met Ser Thr Val Thr
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Arg	Lys	Lys	Thr	Lys	Thr	Ile	Leu	His	Asp	Leu	Asp	Phe	Thr	Val	Glu		
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Thr	Gly	Lys	Ile	Thr	Gly	Leu	Leu	Gly	Pro	Ser	Gly	Ser	Gly	Lys	Thr		
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Gly	Tyr	Val	Thr	Gln	Asn	Ala	Ser	Val	Tyr	His	Asp	Leu	Ser	Val	Ile		
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Glu	Asn	Leu	Lys	Tyr	Phe	Gly	Ala	Leu	Ala	Lys	Gly	Thr	Ser	Thr	Pro		
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Arg	Thr	Pro	Glu	Lys	Ile	Leu	Glu	Val	Leu	Asp	Ile	Ala	Asp	Leu	Ala		
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caa	cgc	caa	gta	tca	aca	cta	tct	ggt	ggg	cag	cgc	ggc	cga	gtc	tcc	547	
Gln	Arg	Gln	Val	Ser	Thr	Leu	Ser	Gly	Gly	Gln	Arg	Gly	Arg	Val	Ser		
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ctt	gga	tgt	gcg	ctt	att	gcc	tca	cca	gaa	ctc	ttg	gtg	atg	gat	gag	595	
Leu	Gly	Cys	Ala	Leu	Ile	Ala	Ser	Pro	Glu	Leu	Leu	Val	Met	Asp	Glu		
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cca	acc	gtg	ggt	ttg	gat	ccc	att	acc	cgg	caa	gca	ctg	tgg	gaa	gag	643	
Pro	Thr	Val	Gly	Leu	Asp	Pro	Ile	Thr	Arg	Gln	Ala	Leu	Trp	Glu	Glu		
			170						175					180			
ttc	acc	acc	atc	gca	aaa	gca	ggt	gct	gga	gtg	gtt	atc	tcc	agt	cac	691	
Phe	Thr	Thr	Ile	Ala	Lys	Ala	Gly	Ala	Gly	Val	Val	Ile	Ser	Ser	His		
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gtg	ttg	gag	gaa	gcc	gcg	cgg	tgc	gac	aac	ctc	att	ttg	ttg	cgt	gat	739	
Val	Leu	Glu	Ala	Ala	Ala	Arg	Cys	Asp	Asn	Leu	Ile	Leu	Leu	Arg	Asp		
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ggt	cgg	atc	atc	tgg	agg	gga	aca	ccc	aca	cgc	ctt	cta	gaa	gat	aca	787	
Gly	Arg	Ile	Ile	Trp	Arg	Gly	Thr	Pro	Thr	Arg	Leu	Leu	Glu	Asp	Thr		
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Gly	Lys	Ser	Ser	Tyr	Glu	Asp	Ala	Phe	Leu	Ala	Ala	Ile	Asp	Gly	Val		
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Arg	Ser																

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 <213> Corynebacterium glutamicum

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 35 40 45
 Gly Ser Gly Lys Thr Thr Leu Met Arg Ala Ile Val Gly Val Gln Asn
 50 55 60
 Phe Asp Gly Thr Leu Glu Val Phe Asp Gln Pro Ala Gly Ala Ala Ser
 65 70 75 80
 Leu Arg Gly Lys Ile Gly Tyr Val Thr Gln Asn Ala Ser Val Tyr His
 85 90 95
 Asp Leu Ser Val Ile Glu Asn Leu Lys Tyr Phe Gly Ala Leu Ala Lys
 100 105 110
 Gly Thr Ser Thr Pro Arg Thr Pro Glu Lys Ile Leu Glu Val Leu Asp
 115 120 125
 Ile Ala Asp Leu Ala Gln Arg Gln Val Ser Thr Leu Ser Gly Gly Gln
 130 135 140
 Arg Gly Arg Val Ser Leu Gly Cys Ala Leu Ile Ala Ser Pro Glu Leu
 145 150 155 160
 Leu Val Met Asp Glu Pro Thr Val Gly Leu Asp Pro Ile Thr Arg Gln
 165 170 175
 Ala Leu Trp Glu Glu Phe Thr Thr Ile Ala Lys Ala Gly Ala Gly Val
 180 185 190
 Val Ile Ser Ser His Val Leu Glu Glu Ala Ala Arg Cys Asp Asn Leu
 195 200 205
 Ile Leu Leu Arg Asp Gly Arg Ile Ile Trp Arg Gly Thr Pro Thr Arg
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<213> *Corynebacterium glutamicum*

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<222> (101) . . (2440)

<223> RXN00829

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Met Gln Lys Ala Asp
1 5

tcc cat gat tgg att tgc gtc cac ggt gcg aat gaa aac aac ctc aaa 163
 Ser His Asp Trp Ile Ser Val His Gly Ala Asn Glu Asn Asn Leu Lys
 10 15 20

aat gtg tgg gtg cgc atc cct aaa agg cgt ctc acc gtg ttc acg ggt 211
Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu Thr Val Phe Thr Gly
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gtg tcg gga tct ggc aag tcc tcg ctg gtg ttc ggc aca att gct gcg 259
Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe Gly Thr Ile Ala Ala
40 45 50

gaa tca cgc cgg ttg atc aac gaa acc tat agc act ttt gtg caa ggt 307
Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser Thr Phe Val Gln Gly
55 60 65

ttc atg ccg tcg atg gca agg ccc gat gtt gac cat ttg gaa ggc atc 355
Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp His Leu Glu Gly Ile
70 75 80 85

acc acg gcg atc atc gtc gat cag gag cag atg ggc gca aac cca cgg 403
Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met Gly Ala Asn Pro Arg
90 95 100

tct acg gtg ggt acc gca act gat gcc acc gcg atg ttg cgc att ttg 451
Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala Met Leu Arg Ile Leu
105 110 115

ttt tcc cga atc gcg gaa cct aac gcg ggt ggc ccg gga gct tat tcc 499
Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly Pro Gly Ala Tyr Ser
120 125 130

ttc aac gtc ccc tct gtt tcc gca tcc ggc gcc atc acg gtg gaa aag 547
Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala Ile Thr Val Glu Lys
135 140 145

ggc gga aac acc aag cgg gag aaa gct acc ttc aaa cgc acg ggt ggc 595
Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe Lys Arg Thr Gly Gly
150 155 160 165

atg tgc cca gcg tgc gag ggc atg ggc agg gcc tca gac atc gac ctc 643
Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala Ser Asp Ile Asp Leu
170 175 180

aaa gag ctt ttc gac gcc tcc ctc tcc ctc aac gac ggc gcc ctg acc 691
Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn Asp Gly Ala Leu Thr
185 190 195

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tcg ggc ctt ttt gat gct gcc aag cgg att aag gat ttc acc gag gaa 787
 Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys Asp Phe Thr Glu Glu
 215 220 225

gaa cgc cac aac ttc ctt tat ctt gag ccc acc aag atg aag atc gct 835
 Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr Lys Met Lys Ile Ala
 230 235 240 245

ggc atc aac atg acc tat gag ggt ctt atc ccc cgc att cag aaa tcc 883
 Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro Arg Ile Gln Lys Ser
 250 255 260

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 265 270 275

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 Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile Asn Gly Lys Asn Ile
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 Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu Ala Lys Trp Ile Lys
 310 315 320 325

acg gtg gaa gcc ccc tcg gtt gct ccc ctg ctc acc gca ctg act gaa 1123
 Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu Thr Ala Leu Thr Glu
 330 335 340

acc ctg gat aac ttc gtg gag atc ggt ttg ggc tat atc caa ctc gat 1171
 Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly Tyr Ile Gln Leu Asp
 345 350 355

cgc ccc gct ggc acg ttg tct ggt ggt gag gca cag cgc acc aag atg 1219
 Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala Gln Arg Thr Lys Met
 360 365 370

atc cgc cat ttg ggc tct gca ttg act gac gtc acc tat gtt ttt gat 1267
 Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val Thr Tyr Val Phe Asp
 375 380 385

gaa ccc acc gcc ggt ttg cac gcc tac gac att gaa cgc atg aac aag 1315
 Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile Glu Arg Met Asn Lys
 390 395 400 405

ttg ctg ctc gat ctt cgc gat aaa ggc aat acc gtt tta gtc gtg gag 1363
 Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr Val Leu Val Val Glu
 410 415 420

cac aag cgc gaa acc atc gcc att gca gat cat gtg gtg gac ctt ggg 1411
 His Lys Pro Glu Thr Ile Ala Ile Ala Asp His Val Val Asp Leu Gly
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Pro Gly Ala Gly Ala Gly Gly Glu Ile Arg Phe Glu Gly Ser Val
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Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly Leu His Phe Asn Asp
455 460 465

cgg gcg tca ttg aag gaa tcc gtg cgt gcg cgg cat ggc gcc ctg gag 1555
Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro His Gly Ala Leu Glu
470 475 480 485

atc cgc ggg gcc gat cga aat aat ttg aac aat gtg gat gtc gat att 1603
Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn Val Asp Val Asp Ile
490 495 500

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Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val Ala Gly Ser Gly Lys
505 510 515

tcc tcg ttg att cat gag att ccg cgt gat gag tcg gtt gtg ttt gtc 1699
Ser Ser Leu Ile His Glu Ile Pro Arg Asp Glu Ser Val Val Phe Val
520 525 530

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Asp Gln Thr Ala Ile His Gly Ser Asn Arg Ser Pro Ala Thr Tyr
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570 575 580

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Cys Lys Gly Ala Gly Ser Val Tyr Val Asp Leu Gly Met Met Ala Gly
585 590 595

gta tct tcg ccg tgt gag gtg tgc gag ggc aag cgt ttt gat gag tcc 1939
Val Ser Ser Pro Cys Glu Val Cys Glu Gly Lys Arg Phe Asp Glu Ser
600 605 610

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Val Leu Asp Tyr His Phe Gly Gly Lys Asp Ile Ala Asp Val Leu Gly
615 620 625

ctg tcg gct gcc aat gcg tat gag ttt ttc gcg gcg aaa gat tca aag 2035
Leu Ser Ala Ala Asn Ala Tyr Glu Phe Phe Ala Ala Lys Asp Ser Lys
630 635 640 645

att ttg cct gcg gca aag atc gca aag agg ctt gtc gac gtc ggc ctc 2083
Ile Leu Pro Ala Ala Lys Ile Ala Lys Arg Leu Val Asp Val Gly Leu
650 655 660

ggc tac atc acc ctc ggc cag ccg ctc acc acg ttg tcc ggc ggt gaa 2131
Gly Tyr Ile Thr Leu Gly Gln Pro Leu Thr Thr Leu Ser Gly Gly Glu
665 670 675

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Thr  Leu  Leu  Asp  Leu  Phe  Asp  Gln  Leu  Val  Asp  Gly  Lys  Ser  Val
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Ile  Val  Ile  Glu  His  His  Leu  Gly  Val  Leu  Ala  His  Ala  Asp  His  Ile
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att  gat  gtc  ggc  cct  ggt  gca  ggt  tct  gat  ggt  ggc  tgg  att  gta  ttc  2371
Ile  Asp  Val  Gly  Pro  Gly  Ala  Gly  Ser  Asp  Gly  Gly  Ser  Ile  Val  Phe
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gag  ggc  agc  ccc  gcg  gaa  ctc  atc  aaa  act  gat  act  cca  aca  gga  cgc  2419
Glu  Gly  Ser  Pro  Ala  Glu  Leu  Ile  Lys  Thr  Asp  Thr  Pro  Thr  Gly  Arg
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Gly  Thr  Ile  Ala  Ala  Glu  Ser  Arg  Arg  Leu  Ile  Asn  Glu  Thr  Tyr  Ser
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Thr  Phe  Val  Gln  Gly  Phe  Met  Pro  Ser  Met  Ala  Arg  Pro  Asp  Val  Asp
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His  Leu  Glu  Gly  Ile  Thr  Thr  Ala  Ile  Ile  Val  Asp  Gln  Glu  Gln  Met
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Gly  Ala  Asn  Pro  Arg  Ser  Thr  Val  Gly  Thr  Ala  Thr  Asp  Ala  Thr  Ala
      100                              105                              110

Met  Leu  Arg  Ile  Leu  Phe  Ser  Arg  Ile  Ala  Glu  Pro  Asn  Ala  Gly  Gly
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Pro  Gly  Ala  Tyr  Ser  Phe  Asn  Val  Pro  Ser  Val  Ser  Ala  Ser  Gly  Ala
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 Lys Arg Thr Gly Gly Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala
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 Ser Asp Ile Asp Leu Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn
 180 185 190
 Asp Gly Ala Leu Thr Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr
 195 200 205
 Arg Met Tyr Ser Glu Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys
 210 215 220
 Asp Phe Thr Glu Glu Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr
 225 230 235 240
 Lys Met Lys Ile Ala Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro
 245 250 255
 Arg Ile Gln Lys Ser Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys
 260 265 270
 His Ile Arg Ala Phe Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro
 275 280 285
 Ala Cys Gly Gly Thr Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile
 290 295 300
 Asn Gly Lys Asn Ile Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu
 305 310 315 320
 Ala Lys Trp Ile Lys Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu
 325 330 335
 Thr Ala Leu Thr Glu Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly
 340 345 350
 Tyr Ile Gln Leu Asp Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala
 355 360 365
 Gln Arg Thr Lys Met Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val
 370 375 380
 Thr Tyr Val Phe Asp Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile
 385 390 395 400
 Glu Arg Met Asn Lys Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr
 405 410 415
 Val Leu Val Val Glu His Lys Pro Glu Thr Ile Ala Ile Ala Asp His
 420 425 430
 Val Val Asp Leu Gly Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg
 435 440 445
 Phe Glu Gly Ser Val Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly
 450 455 460
 Leu His Phe Asn Asp Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro

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465 470 475 480
 His Gly Ala Leu Glu Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn
 485 490 495
 Val Asp Val Asp Ile Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val
 500 505 510
 Ala Gly Ser Gly Lys Ser Ser Leu Ile His Glu Ile Pro Arg Asp Glu
 515 520 525
 Ser Val Val Phe Val Asp Gln Thr Ala Ile His Gly Ser Asn Arg Ser
 530 535 540
 Asn Pro Ala Thr Tyr Thr Gly Met Leu Asp Ser Ile Arg Lys Ala Phe
 545 550 555 560
 Ala Lys Ala Asn Asp Val Lys Pro Ala Leu Phe Ser Pro Asn Ser Glu
 565 570 575
 Gly Ala Cys Pro Asn Cys Lys Gly Ala Gly Ser Val Tyr Val Asp Leu
 580 585 590
 Gly Met Met Ala Gly Val Ser Ser Pro Cys Glu Val Cys Glu Gly Lys
 595 600 605
 Arg Phe Asp Glu Ser Val Leu Asp Tyr His Phe Gly Gly Lys Asp Ile
 610 615 620
 Ala Asp Val Leu Gly Leu Ser Ala Ala Asn Ala Tyr Glu Phe Phe Ala
 625 630 635 640
 Ala Lys Asp Ser Lys Ile Leu Pro Ala Ala Lys Ile Ala Lys Arg Leu
 645 650 655
 Val Asp Val Gly Leu Gly Tyr Ile Thr Leu Gly Gln Pro Leu Thr Thr
 660 665 670
 Leu Ser Gly Gly Glu Arg Gln Arg Leu Lys Leu Ala Thr His Met Ala
 675 680 685
 Asp Lys Ala Thr Thr Phe Ile Leu Asp Glu Pro Thr Thr Gly Leu His
 690 695 700
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 Asp Gly Lys Ser Val Ile Val Ile Glu His His Leu Gly Val Leu Ala
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 His Ala Asp His Ile Ile Asp Val Gly Pro Gly Ala Gly Ser Asp Gly
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 <213> *Corynebacterium glutamicum*

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 <222> (1)..(255)
 <223> FRXA00829

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 Leu Asp Leu Phe Asp Gln Leu Val Asp Asp Gly Lys Ser Val Ile Val
 20 25 30
 atc gaa cac cac ctg ggc gtg ctg gct cac gct gac cac atc att gat 144
 Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile Ile Asp
 35 40 45
 gtc ggc cct ggt gca ggt tct gat ggt ggc tcg att gta ttc gag ggc 192
 Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe Glu Gly
 50 55 60
 agc ccc gcg gaa ctg atc aaa act gat act cca aca gga cgc cac ctt 240
 Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg His Leu
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 Lys Ala Tyr Val Asp
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 <212> PRT
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 Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile Ile Asp
 35 40 45
 Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe Glu Gly
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<210> 149

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				1																
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Phe	Met	Pro	Ser	Met	Ala	Arg	Pro	Asp	Val	Asp	His	Leu	Glu	Gly	Ile					
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acc	acg	gcg	atc	atc	gtc	gat	cag	gag	cag	atg	ggc	gca	aac	cca	cgg	403				
Thr	Thr	Ala	Ile	Ile	Val	Asp	Gln	Glu	Gln	Met	Gly	Ala	Asn	Pro	Arg					
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Met	Cys	Pro	Ala	Cys	Glu	Gly	Met	Gly	Arg	Ala	Ser	Asp	Ile	Asp	Leu					
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tcg Ser	ggc Gly 215	ctt Leu	ttt Phe	gat Asp	gct Ala	gcc Ala 220	aag Lys	cgc Pro	att Ile	aag Lys 225	gat Asp	ttc Phe	acc Thr	gag Glu	gaa Glu	787
gaa Glu 230	cgc Arg	cac His	aac Asn	ttc Phe	ctt Leu 235	tat Tyr	ctt Leu	gag Glu	ccc Pro	acc Thr 240	aag Lys	atg Met	aag Lys	atc Ile	gct Ala 245	835
ggc Gly	atc Ile	aac Asn	atg Met	acc Thr 250	tat Tyr	gag Glu	ggg Gly	ctt Leu 255	atc Ile	ccc Pro	cgc Arg	att Ile	cag Gln	aaa Lys 260	tcc Ser	883
atg Met	ttg Leu	tct Ser	aag Ser 265	gat Asp	cgc Arg	gaa Glu	ggc Gly 270	atg Met	cag Gln	aag Lys	cat His	att Ile 275	cgt Arg 275	gcg Ala	ttc Phe	931
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cga Arg	tta Ala 295	gcg Ala	cca Pro	cat His	gcc Ala	ttg Leu 300	gag Glu	tcc Ser	aag Lys	atc Ile	aat Asn 305	ggc Gly	aaa Lys	aac Asn	atc Ile	1027
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acg Thr	gtg Val	gaa Glu	gcc Ala	ccc Pro 330	tcg Ser	gtt Val	gct Ala	ccc Pro	ctg Leu 335	ctc Leu	acc Thr	gca Ala	ctg Leu	act Thr 340	gaa Glu	1123
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cgc Arg	ccc Pro	gct Ala 360	ggc Gly	acg Thr	ttg Leu	tct Ser	ggg Gly 365	ggg Gly	gag Glu	gca Ala	cag Gln	cgc Arg 370	acc Thr	aag Lys	atg Met	1219
atc Ile	cgc Arg 375	cat His	ttg Leu	ggc Gly	tct Ser	gca Ala 380	ttg Leu	act Asp	gac Thr	gtc Val	acc Thr 385	tat Tyr	gtt Val	ttt Phe	gat Asp	1267
gaa Glu 390	ccc Pro	acc Thr	gcc Ala	ggg Gly 395	ttg Leu	cac His	gcc Ala	tac Tyr	gac Asp	att Ile 400	gaa Glu	cgc Arg	atg Met	aac Asn	aag Lys 405	1315
ttg Leu	ctg Leu	ctc Leu	gat Asp	ctt Leu 410	cgc Arg	gat Asp	aaa Lys	ggc Gly	aat Asn 415	acc Thr	gtt Val	tta Leu	gtc Val	gtg Val 420	gag Glu	1363
cac His	aag Lys	ccg Pro	gaa Glu	acc Thr	atc Ile	gcc Ala	att Ile	gca Ala	gat Asp	cat His	gtg Val	gtg Val	gac Leu	ctt Leu	ggg Gly	1411

425 430 435
 cca ggt gca ggc gcg ggt gga ggt gaa att cgg ttt gag ggg agc gtc 1459
 Pro Gly Ala Gly Ala Gly Gly Glu Ile Arg Phe Glu Gly Ser Val
 440 445 450
 gac aag ctt aaa gac agc gac acc gtg act ggc ctc cat ttt aat gac 1507
 Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly Leu His Phe Asn Asp
 455 460 465
 cgg gcg tca ttg aag gaa tcc gtg cgt gcg cgg cat ggc gcc ctg gag 1555
 Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro His Gly Ala Leu Glu
 470 475 480 485
 atc cgc ggg gcc gat cga aat aat ttg aac aat gtg gat gtc gat att 1603
 Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn Val Asp Val Asp Ile
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 ccg ctc ggc gtg ttc acg gcg att tcc ggc gtt gca ggt tcg ggt aag 1651
 Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val Ala Gly Ser Gly Lys
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 tcc tcg ttg att 1663
 Ser Ser Leu Ile
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 <213> *Corynebacterium glutamicum*
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 Thr Val Phe Thr Gly Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe
 35 40 45
 Gly Thr Ile Ala Ala Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser
 50 55 60
 Thr Phe Val Gln Gly Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp
 65 70 75 80
 His Leu Glu Gly Ile Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met
 85 90 95
 Gly Ala Asn Pro Arg Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala
 100 105 110
 Met Leu Arg Ile Leu Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly
 115 120 125
 Pro Gly Ala Tyr Ser Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala
 130 135 140
 Ile Thr Val Glu Lys Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe

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145 150 155 160
 Lys Arg Thr Gly Gly Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala
 165 170 175
 Ser Asp Ile Asp Leu Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn
 180 185 190
 Asp Gly Ala Leu Thr Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr
 195 200 205
 Arg Met Tyr Ser Glu Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys
 210 215 220
 Asp Phe Thr Glu Glu Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr
 225 230 235 240
 Lys Met Lys Ile Ala Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro
 245 250 255
 Arg Ile Gln Lys Ser Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys
 260 265 270
 His Ile Arg Ala Phe Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro
 275 280 285
 Ala Cys Gly Gly Thr Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile
 290 295 300
 Asn Gly Lys Asn Ile Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu
 305 310 315 320
 Ala Lys Trp Ile Lys Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu
 325 330 335
 Thr Ala Leu Thr Glu Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly
 340 345 350
 Tyr Ile Gln Leu Asp Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala
 355 360 365
 Gln Arg Thr Lys Met Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val
 370 375 380
 Thr Tyr Val Phe Asp Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile
 385 390 395 400
 Glu Arg Met Asn Lys Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr
 405 410 415
 Val Leu Val Val Glu His Lys Pro Glu Thr Ile Ala Ile Ala Asp His
 420 425 430
 Val Val Asp Leu Gly Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg
 435 440 445
 Phe Glu Gly Ser Val Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly
 450 455 460
 Leu His Phe Asn Asp Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro
 465 470 475 480

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His Gly Ala Leu Glu Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn
485 490 495

Val Asp Val Asp Ile Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val
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Ala Gly Ser Gly Lys Ser Ser Leu Ile
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<211> 864

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(841)

<223> RXA00995

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Met Asn Pro His Tyr
1 5

ctg ctt gcc acg gtc aaa cga gtc ctg ctg cag ctg aaa gcc gat aaa 163
Leu Leu Ala Thr Val Lys Arg Val Leu Leu Gln Leu Lys Ala Asp Lys
10 15 20

cgt tcc atc gcg ctg att ctt cta gca ccc gtg gcg ttg atg tgg ctg 211
Arg Ser Ile Ala Leu Ile Leu Leu Ala Pro Val Ala Leu Met Ser Leu
25 30 35

ttt tat tac atg tat tcc tcc aca ccg gca ggc acc cag ctg ttt aag 259
Phe Tyr Tyr Met Tyr Ser Ser Thr Pro Ala Gly Thr Gln Leu Phe Lys
40 45 50

acc att tcc acg gtc atg atc gca gtg ttc ccc ttg atg ctc atg ttt 307
Thr Ile Ser Thr Val Met Ile Ala Val Phe Pro Leu Met Leu Met Phe
55 60 65

ttg atg acg tgg gtg acg atg caa aga gaa cgc aac gct gga acg ctc 355
Leu Met Thr Ser Val Thr Met Gln Arg Glu Arg Asn Ala Gly Thr Leu
70 75 80 85

gag cgc ttg tgg acc acg aac att cac cgc gtt gat ttg atc ggt ggc 403
Glu Arg Leu Trp Thr Thr Asn Ile His Arg Val Asp Leu Ile Gly Gly
90 95 100

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Tyr Gly Val Ala Phe Gly Ile Met Ala Val Ala Gln Ser Leu Leu Met
105 110 115

gtg ctc acc ctt cgg tat ctc ctg ggt gtg gaa acc gaa tgg gag tgg 499
Val Leu Thr Leu Arg Tyr Leu Leu Gly Val Glu Thr Glu Ser Glu Trp
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 Leu Gly Leu Leu Ser Ser Ala Phe Ala Ser Thr Glu Phe Gln Ala Ile
 150 155 160 165
 caa acg ctg ccg ttg ctt att ttg ccc cag ttc cta ttg tgc ggt ttg 643
 Gln Thr Leu Pro Leu Leu Ile Leu Pro Gln Phe Leu Leu Cys Gly Leu
 170 175 180
 ctg atc cca cgg gat gat ctg-ccg gat gtg ttg cgc tgg gtt tct aat 691
 Leu Ile Pro Arg Asp Asp Leu Pro Asp Val Leu Arg Trp Val Ser Asn
 185 190 195
 gtg ttg ccg ctg tcc tat gca gtt gat gca gcg ctt gag gcc tca cgg 739
 Val Leu Pro Leu Ser Tyr Ala Val Asp Ala Ala Leu Glu Ala Ser Arg
 200 205 210
 acg gga atc gga cag caa gta gtg gtc aac att gcc atc tgc gcc gcg 787
 Thr Gly Ile Gly Gln Gln Val Val Val Asn Ile Ala Ile Cys Ala Ala
 215 220 225
 ttt gcc gtg agc ttc ctg ctg gtg gcg gcg cta tcg atg ccg aga atg 835
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 Thr Arg

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 <213> *Corynebacterium glutamicum*

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 Ala Leu Met Ser Leu Phe Tyr Tyr Met Tyr Ser Ser Thr Pro Ala Gly
 35 40 45
 Thr Gln Leu Phe Lys Thr Ile Ser Thr Val Met Ile Ala Val Phe Pro
 50 55 60
 Leu Met Leu Met Phe Leu Met Thr Ser Val Thr Met Gln Arg Glu Arg
 65 70 75 80
 Asn Ala Gly Thr Leu Glu Arg Leu Trp Thr Thr Asn Ile His Arg Val
 85 90 95
 Asp Leu Ile Gly Gly Tyr Gly Val Ala Phe Gly Ile Met Ala Val Ala
 100 105 110
 Gln Ser Leu Leu Met Val Leu Thr Leu Arg Tyr Leu Leu Gly Val Glu
 115 120 125

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Thr Glu Ser Glu Trp Trp Ile Ser Thr Leu Ile Ala Ala Ile Thr Gly
130 135 140

Leu Ile Gly Val Ser Leu Gly Leu Leu Ser Ser Ala Phe Ala Ser Thr
145 150 155 160

Glu Phe Gln Ala Ile Gln Thr Leu Pro Leu Leu Ile Leu Pro Gln Phe
165 170 175

Leu Leu Cys Gly Leu Leu Ile Pro Arg Asp Asp Leu Pro Asp Val Leu
180 185 190

Arg Trp Val Ser Asn Val Leu Pro Leu Ser Tyr Ala Val Asp Ala Ala
195 200 205

Leu Glu Ala Ser Arg Thr Gly Ile Gly Gln Gln Val Val Val Asn Ile
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Ser Met Pro Arg Met Thr Arg
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<210> 153

<211> 1353

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> {101}..(1330)

<223> RXN00803

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Met Gly Val Ser Ala
1 5

ctt aac atg tct gac atg gtg gcg aac aaa cgg gca cag cgt aaa gtc 163
Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg Ala Gln Arg Lys Val
10 15 20

tgg cta gcg gta gct tta tcg gtc ttt acg gtc gcg tgg ggt ggc aat 211
Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val Ala Trp Gly Gly Asn
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gaa ttc act ccc ttg ctg gtg ttt tac cga ggt gaa ggg ttc ttt agc 259
Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly Glu Gly Phe Phe Ser
40 45 50

aac ctg ttc atc gac ctt ttg ctg gtg ttt tat gcc atc gga gta gcg 307
Asn Leu Phe Ile Asp Leu Leu Val Phe Tyr Ala Ile Gly Val Ala
55 60 65

gta ggt ttg ctg gca gct ggt cct tta tct gac cgc tat ggc cga cgt 355
Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp Arg Tyr Gly Arg Arg

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att gcc tcg ggt gaa gaa acc gcc atc ctg att gcc att ggt cga gtg Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile Ala Ile Gly Arg Val			451
ctg tcg gga att tcg gtg ggc atg gtg atg aca gcg gga ggt tcc tgg Leu Ser Gly Ile Ser Val Gly Met Val Met Thr Ala Gly Gly Ser Trp			499
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gct ggt gca aaa cgc gca tcg atg tct ttg acc ggt ggt ttt gcg ctc Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr Gly Gly Phe Ala Leu			595
ggc cca gcg ctt gct ggt gtg atg gca cag tgg ctg cca cta cct gga Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp Leu Pro Leu Pro Gly			643
cag ttg gca tat gtt ttg cac att att ctc act ctg att ttg ttc ccg Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr Leu Ile Leu Phe Pro			691
ttg ctt att aca gcg ccg gaa act cgt caa tca gcg cac ctg aaa act Leu Leu Ile Thr Ala Pro Glu Thr Arg Gln Ser Ala His Leu Lys Thr			739
aag gga tca ttc tgg tca gat gtg ctt gtg cca tct gca cta gac aag Lys Gly Ser Phe Trp Ser Asp Val Leu Val Pro Ser Ala Leu Asp Lys			787
cga ttc ttg ttt gtg gtt gct cca att gga ccg tgg gtt ttc ggt gcg Arg Phe Leu Phe Val Val Ala Pro Ile Gly Pro Trp Val Phe Gly Ala			835
gcc ttc act gcc tac gca gtt ttg ccg tcg cag ctg cgt gac atg gtt Ala Phe Thr Ala Tyr Ala Val Leu Pro Ser Gln Leu Arg Asp Met Val			883
tct gca ccc gtt gcg tat tct gcg ctg atc gct ttg gtt acc tta ggt Ser Ala Pro Val Ala Tyr Ser Ala Leu Ile Ala Leu Val Thr Leu Gly			931
tct gga ttt ggt atc caa caa ttc ggt cct caa atc atg ggc acc tct Ser Gly Phe Gly Ile Gln Gln Phe Gly Pro Gln Ile Met Gly Thr Ser			979
aaa act cgc ggg ccg att ttg gcc atg ttc gtc aca gtc atc ggc atg Lys Thr Arg Gly Pro Ile Leu Ala Met Phe Val Thr Val Ile Gly Met			1027
atc ggc gcg gtg atc gtg gtg atg aac cct cat cca tgg tgg gcg cta Ile Gly Ala Val Ile Val Val Met Asn Pro His Pro Trp Trp Ala Leu			1075

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 Val Gly Cys Met Ala Leu Gly Leu Ser Tyr Gly Leu Cys Met Phe Met
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ggg ttg gcg gaa act caa aac att gct cca cct att gat atg gca ggc 1171
 Gly Leu Ala Glu Thr Gln Asn Ile Ala Pro Pro Ile Asp Met Ala Gly
 345 350 355

ctg acg ggt att ttc tac tgc ctg acg tac gta ggt atg gtc ttt cca 1219
 Leu Thr Gly Ile Phe Tyr Cys Leu Thr Tyr Val Gly Met Val Phe Pro
 360 365 370

gcc ttg atg acc tgg ttg aat caa tgg ctc agt tac ccg ttc atg ctg 1267
 Ala Leu Met Thr Trp Leu Asn Gln Trp Leu Ser Tyr Pro Phe Met Leu
 375 380 385

gcc ttt ggt gcg gtg atg gca act att tgt ctg atc att gtg agt ttt 1315
 Gly Phe Gly Ala Val Met Ala Thr Ile Cys Leu Tyr Ile Val Ser Phe
 390 395 400 405

agt gca cgc cga ttc tgagaaacaa cttaaagtga cca 1353
 Ser Ala Arg Arg Phe
 410

<210> 154
 <211> 410
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 154
 Met Gly Val Ser Ala Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg
 1 5 10 15

Ala Gln Arg Lys Val Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val
 20 25 30

Ala Trp Gly Gly Asn Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly
 35 40 45

Glu Gly Phe Phe Ser Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr
 50 55 60

Ala Ile Gly Val Ala Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp
 65 70 75 80

Arg Tyr Gly Arg Arg Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile
 85 90 95

Leu Gly Ser Ala Leu Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile
 100 105 110

Ala Ile Gly Arg Val Leu Ser Gly Ile Ser Val Gly Met Val Met Thr
 115 120 125

Ala Gly Gly Ser Trp Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro
 130 135 140

Gly Val Lys Thr Ser Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr
 145 150 155 160

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Gly Gly Phe Ala Leu Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp
 165 170 175
 Leu Pro Leu Pro Gly Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr
 180 185 190
 Leu Ile Leu Phe Pro Leu Leu Ile Thr Ala Pro Glu Thr Arg Gln Ser
 195 200 205
 Ala His Leu Lys Thr Lys Gly Ser Phe Trp Ser Asp Val Leu Val Pro
 210 215 220
 Ser Ala Leu Asp Lys Arg Phe Leu Phe Val Val Ala Pro Ile Gly Pro
 225 230 235 240
 Trp Val Phe Gly Ala Ala Phe Thr Ala Tyr Ala Val Leu Pro Ser Gln
 245 250 255
 Leu Arg Asp Met Val Ser Ala Pro Val Ala Tyr Ser Ala Leu Ile Ala
 260 265 270
 Leu Val Thr Leu Gly Ser Gly Phe Gly Ile Gln Gln Phe Gly Pro Gln
 275 280 285
 Ile Met Gly Thr Ser Lys Thr Arg Gly Pro Ile Leu Ala Met Phe Val
 290 295 300
 Thr Val Ile Gly Met Ile Gly Ala Val Ile Val Val Met Asn Pro His
 305 310 315 320
 Pro Trp Trp Ala Leu Val Gly Cys Met Ala Leu Gly Leu Ser Tyr Gly
 325 330 335
 Leu Cys Met Phe Met Gly Leu Ala Glu Thr Gln Asn Ile Ala Pro Pro
 340 345 350
 Ile Asp Met Ala Gly Leu Thr Gly Ile Phe Tyr Cys Leu Thr Tyr Val
 355 360 365
 Gly Met Val Phe Pro Ala Leu Met Thr Trp Leu Asn Gln Trp Leu Ser
 370 375 380
 Tyr Pro Phe Met Leu Gly Phe Gly Ala Val Met Ala Thr Ile Cys Leu
 385 390 395 400
 Ile Ile Val Ser Phe Ser Ala Arg Arg Phe
 405 410

<210> 155

<211> 703

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> FRXA00803

<400> 155

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cggccgtttc gttaaagatt ggtctggcca ttctctccat atg ggg gtg tcc gcg 115
Met Gly Val Ser Ala
1 5

ctt aac atg tct gac atg gtg gcg aac aaa cgg gca cag cgt aaa gtc 163
Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg Ala Gln Arg Lys Val
10 15 20

tgg cta gcg gta gct tta tcg gtc ttt acg gtc gcg tgg ggt ggc aat 211
Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val Ala Trp Gly Gly Asn
25 30 35

gaa ttc act ccc ttg ctg gtg ttt tac cga ggt gaa ggg ttc ttt agc 259
Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly Glu Gly Phe Phe Ser
40 45 50

aac ctg ttc atc gac ctt ttg ctg gtg ttt tat gcc atc gga gta gcg 307
Asn Leu Phe Ile Asp Leu Leu Val Phe Tyr Ala Ile Gly Val Ala
55 60 65

gta ggt ttg ctg gca gct ggt cct tta tct gac cgc tat ggc cga cgt 355
Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp Arg Tyr Gly Arg Arg
70 75 80 85

gcc gtc atg ttg cct gcg cca ttg atc gcg atc ttg ggt tcc gcg ttg 403
Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile Leu Gly Ser Ala Leu
90 95 100

att gcc tcg ggt gaa gaa acc gcc atc ctg att gcc att ggt cga gtg 451
Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile Ala Ile Gly Arg Val
105 110 115

ctg tcg gga att tcg gtg ggc atg gtg atg aca gcg gga ggt tcc tgg 499
Leu Ser Gly Ile Ser Val Gly Met Val Met Thr Ala Gly Gly Ser Trp
120 125 130

att aag gag ctt tca tcg tcg cgg ttt gag cca ggg gtg aaa acc agt 547
Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro Gly Val Lys Thr Ser
135 140 145

gct ggt gca aaa cgc gca tcg atg tct ttg acc ggt ggt ttt gcg ctc 595
Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr Gly Gly Phe Ala Leu
150 155 160 165

ggc cca gcg ctt gct ggt gtg atg gca cag tgg ctg cca caa cct gga 643
Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp Leu Pro Gln Pro Gly
170 175 180

cag ttg gca tat gtt ttg cac att att ctc act ctg att ttg ttc ccg 691
Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr Leu Ile Leu Phe Pro
185 190 195

ttg ctt att aca 703
Leu Leu Ile Thr
200

<210> 156
<211> 201

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 156

Met Gly Val Ser Ala Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg
 1 5 10 15

Ala Gln Arg Lys Val Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val
 20 25 30

Ala Trp Gly Gly Asn Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly
 35 40 45

Glu Gly Phe Phe Ser Asn Leu Phe Ile Asp Leu Leu Val Phe Tyr
 50 55 60

Ala Ile Gly Val Ala Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp
 65 70 75 80

Arg Tyr Gly Arg Arg Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile
 85 90 95

Leu Gly Ser Ala Leu Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile
 100 105 110

Ala Ile Gly Arg Val Leu Ser Gly Ile Ser Val Gly Met Val Met Thr
 115 120 125

Ala Gly Gly Ser Trp Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro
 130 135 140

Gly Val Lys Thr Ser Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr
 145 150 155 160

Gly Gly Phe Ala Leu Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp
 165 170 175

Leu Pro Gln Pro Gly Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr
 180 185 190

Leu Ile Leu Phe Pro Leu Leu Ile Thr
 195 200

<210> 157

<211> 1014

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(991)

<223> RXA01407

<400> 157

atccggggaa cggatcccaa agatctcctt gatgccatcg cggttttaac ctggccagct 60

ctgggtgccc cagtgatgcg cccacttctg ggagggtcttc ttg caa gat acc att 115
 Leu Gln Asp Thr Ile
 1 5

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ggt tgc cga tgg atc ttc ctc ctc aac gtg ccc tta gga atc atc gcg 163
 Gly Cys Arg Trp Ile Phe Leu Leu Asn Val Pro Leu Gly Ile Ile Ala
 10 15 20

atc atg gct gga cta ttc atc cag ccc aag aac acg gcc gtg aat gtg 211
 Ile Met Ala Gly Leu Phe Ile Gln Pro Lys Asn Thr Ala Val Asn Val
 25 30 35

aag cga ttt gat cgg cca ggt ttc ctc gcc gca atg ctg gtg atg gtg 259
 Lys Arg Phe Asp Arg Pro Gly Phe Leu Gly Ala Met Leu Val Met Val
 40 45 50

gcg caa gcc gtg att gcg gag tta att tgc agc aga agt ccg gcc gca 307
 Ala Gln Ala Val Ile Ala Glu Leu Ile Cys Ser Arg Ser Pro Ala Ala
 55 60 65

ctt act atc tgt gca tgc ctc gtc tta agt gct gcg gtg gta tgc ggt 355
 Leu Thr Ile Cys Ala Cys Leu Val Leu Ser Ala Ala Val Val Cys Gly
 70 75 80 85

ttt gta gtg cgc tgg ctg cga gtt cca gcc cga ctt ttt gat ctc agc 403
 Phe Val Val Arg Trp Leu Arg Val Pro Gly Arg Leu Phe Asp Leu Ser
 90 95 100

atc atg cgc atc cca ggt ttc cga gtg ggt aat tcc tcc gga agt atc 451
 Ile Met Arg Ile Pro Gly Phe Arg Val Gly Asn Ser Ser Gly Ser Ile
 105 110 115

tac cgc ttg gta atc acc gca gca cca ttc atg ttc act ttg ctc ttc 499
 Tyr Arg Leu Val Ile Thr Ala Ala Pro Phe Met Phe Thr Leu Leu Phe
 120 125 130

caa gtg gcg ttt ggg tgg tct gca aca tta gcg ggt gcc atg gtg gtc 547
 Gln Val Ala Phe Gly Trp Ser Ala Thr Leu Ala Gly Ala Met Val Val
 135 140 145

gca cta ttc gca gcc aac gtg gca atc aaa cct ttc acc acg ccg atc 595
 Ala Leu Phe Ala Gly Asn Val Ala Ile Lys Pro Phe Thr Thr Pro Ile
 150 155 160 165

att aaa cgc tgg aat ttc aaa cca gta ctg gtc ttt tct aac gct gct 643
 Ile Lys Arg Trp Asn Phe Lys Pro Val Leu Val Phe Ser Asn Ala Ala
 170 175 180

gcc gcc ttg gta ttg gca act ttt ttg ttc gtt cgt gca gat acc cca 691
 Gly Ala Leu Val Leu Ala Thr Phe Leu Phe Val Arg Ala Asp Thr Pro
 185 190 195

ctg gtt ctc atc gtg ctg ctg ctc ttt gtt tgg gcc gca tta agg tcc 739
 Leu Val Leu Ile Val Leu Leu Leu Phe Val Ser Gly Ala Leu Arg Ser
 200 205 210

ctc ggt ttc agc gcc tac aac acc ttg cag ttt gtc gat atc tca cca 787
 Leu Gly Phe Ser Ala Tyr Asn Thr Leu Gln Phe Val Asp Ile Ser Pro
 215 220 225

gaa caa acc agc aac gcc aac gtg tta tca gca acc ctg cac caa cta 835
 Glu Gln Thr Ser Asn Ala Asn Val Leu Ser Ala Thr Leu His Gln Leu
 230 235 240 245

gcc atg tct ttg ggt att gcg gta gca gtc atc gcc atg tcc ctt gca 883

002200 802E960

Gly Met Ser Leu Gly Ile Ala Val Ala Val Ile Ala Met Ser Leu Ala
 250 255 260

ccc acc gcc aac tgg gca ttc cca ctg gca gca gcg ttg ttc ctc att 931
 Pro Thr Ala Asn Trp Ala Phe Pro Leu Ala Ala Ala Leu Phe Leu Ile
 265 270 275

cct cta atc gcc gca cta tct ttg cct cgc gac gcc ggt gcc cga gcc 979
 Pro Leu Ile Gly Ala Leu Ser Leu Pro Arg Asp Gly Gly Ala Arg Ala
 280 285 290

ttt tcc tcc tct tagaaaccca cttctgaaag gta 1014
 Phe Ser Ser Ser
 295

<210> 158
 <211> 297
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 158
 Leu Gln Asp Thr Ile Gly Cys Arg Trp Ile Phe Leu Leu Asn Val Pro
 1 5 10 15

Leu Gly Ile Ile Ala Ile Met Ala Gly Leu Phe Ile Gln Pro Lys Asn
 20 25 30

Thr Ala Val Asn Val Lys Arg Phe Asp Arg Pro Gly Phe Leu Gly Ala
 35 40 45

Met Leu Val Met Val Ala Gln Ala Val Ile Ala Glu Leu Ile Cys Ser
 50 55 60

Arg Ser Pro Ala Ala Leu Thr Ile Cys Ala Cys Leu Val Leu Ser Ala
 65 70 75 80

Ala Val Val Cys Gly Phe Val Val Arg Trp Leu Arg Val Pro Gly Arg
 85 90 95

Leu Phe Asp Leu Ser Ile Met Arg Ile Pro Gly Phe Arg Val Gly Asn
 100 105 110

Ser Ser Gly Ser Ile Tyr Arg Leu Val Ile Thr Ala Ala Pro Phe Met
 115 120 125

Phe Thr Leu Leu Phe Gln Val Ala Phe Gly Trp Ser Ala Thr Leu Ala
 130 135 140

Gly Ala Met Val Val Ala Leu Phe Ala Gly Asn Val Ala Ile Lys Pro
 145 150 155 160

Phe Thr Thr Pro Ile Ile Lys Arg Trp Asn Phe Lys Pro Val Leu Val
 165 170 175

Phe Ser Asn Ala Ala Gly Ala Leu Val Leu Ala Thr Phe Leu Phe Val
 180 185 190

Arg Ala Asp Thr Pro Leu Val Leu Ile Val Leu Leu Leu Phe Val Ser
 195 200 205

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Gly	Ala	Leu	Arg	Ser	Leu	Gly	Phe	Ser	Asn	Tyr	Thr	Leu	Gln	Phe
210						215								
Val	Asp	Ile	Ser	Pro	Glu	Gln	Thr	Ser	Asn	Ala	Asn	Val	Leu	Ser
225					230					235				240
Thr	Leu	His	Gln	Leu	Gly	Met	Ser	Leu	Gly	Ile	Ala	Val	Ala	Val
				245					250					255
Ala	Met	Ser	Leu	Ala	Pro	Thr	Ala	Asn	Trp	Ala	Phe	Pro	Leu	Ala
				260				265					270	
Ala	Leu	Phe	Leu	Ile	Pro	Leu	Ile	Gly	Ala	Leu	Ser	Leu	Pro	Arg
	275						280					285		Asp
Gly	Gly	Ala	Arg	Ala	Phe	Ser	Ser							
290					295									

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<210> 159
<211> 324
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(301)  
<223> RXA01408
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<400> 159
ggatagaggt tatctgaaa ctaccaagac gttttctttt ctttagatct aaggaggaga 60

gaccgtcttt caccctttca tctgattgga catcgacgcc atg cgc aat gat cgg 115
Met Arg Asn Asp Arg
1 5

tcc ttt agc gtt ccc att gcg cta ctt gcc gcg gga gca ctg ttt cta 163
Ser Phe Ser Val Pro Ile Ala Leu Leu Ala Ala Gly Ala Leu Phe Leu
10 15 20

gaa atc ctc gac ggc acc atc ctg aca acc gca gtg cca gct att gct 211
Glu Ile Leu Asp Gly Thr Ile Leu Thr Thr Ala Val Pro Ala Ile Ala
25 30 35

cgt gac ttc ggt att gac gcc gtg gat gtc agc att gca ctg gtt gct 259
Arg Asp Phe Gly Ile Asp Ala Val Asp Val Ser Ile Ala Leu Val Ala
40 45 50

tac ttg gca gcc gca gca gct ggc att ccg ctg cag ggt ggc 301
Tyr Leu Ala Ala Ala Ala Gly Ile Pro Leu Gln Gly Gly
55 60 65

tagcagatcg atttggtgtg cgc 324

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<210> 160
<211> 67
<212> PRT
<213> Corynebacterium glutamicum
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<400> 160

Figure 6

<220>
<221> CDS
<222> (101)..(1252)
<223> RXN01922

<400> 161
acactcctttt ggtcacctgg tttggttgag ggaacacagac gcgccaaagaa cccaagaaat 60
cccaagaaaa catgctgcctt atgaattaaa gtgagcacccc atg aga tca gga aac 115
Met Arg Ser Gly Asn
1 5
gcc aat cgc gtc ttc ata ggt gtt acc atc ctg ctg ttt act gca gga 163
Ala Asn Arg Val Phe Ile Gly Val Thr Ile Leu Leu Phe Thr Ala Gly
10 15 20
tgg gca gcc aat ttc cgc tca gtg ttg gtg ttg atc cgt gaa caa 211
Trp Ala Ala Asn His Phe Ala Ser Val Leu Val Leu Ile Arg Glu Gln
25 30 35
tta gac gat tca agc gtg ctg gtc aac ggc gct ttt ggt att tat gca 259
Leu Asp Val Ser Ser Val Leu Val Asn Gly Ala Phe Gly Ile Tyr Ala
40 45 50
ctg gga ctt ctt cca agt ttg ctc gca ggc ggt gtg ctt gcc gac cgt 307
Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly Val Leu Ala Asp Arg
55 60 65
ttt ggt gcc cgc atg gtg gta ctc acc gga ggt gta ctt tct cgq ctt 355
Phe Gly Ala Arg Met Val Val Leu Thr Gly Gly Val Leu Ser Ala Leu
70 75 80 85
gga aac ctt tct ctt tta gcg ttt cat gat ggt cct tcg ctc ctg gta 403
Gly Asn Leu Ser Leu Leu Ala Phe His Asp Gly Pro Ser Leu Leu Val
90 95 100
gga cga ttc atc gtt ggt ctg gcc gtt gga tta gtc gtc agc gcg gcc 451
Gly Arg Phe Ile Val Gly Leu Gly Val Gly Leu Val Val Ser Ala Gly
105 110 115

2023

acc gca tgg gcg ggc aga ttg cgc gga gca agc ggc gtg aca ttg gcc 499
 Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala Ser Gly Val Thr Leu Ala
 120 125 130

ggc att att ctg acc gcc ggt ttc atg atg ggg ccg att gtg aca agt 547
 Gly Ile Ile Leu Thr Ala Gly Phe Met Met Gly Pro Ile Val Thr Ser
 135 140 145

ggg ttg ggg atg gcg tcg aca agc att att acg ccc ttt gcc ata agc 595
 Gly Leu Gly Met Ala Ser Thr Ser Ile Ile Thr Pro Phe Ala Ile Ser
 150 155 160 165

gtt gcc ctc tcg ctg atc gcg gtg gtt gtg gga ttt gcg ctt ggc gat 643
 Val Ala Leu Ser Leu Ile Ala Val Val Val Gly Phe Ala Leu Gly Asp
 170 175 180

gcc cgc agc acc ccg agc gca ctt ggc gca tcc agc gga atc aaa cac 691
 Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala Ser Ser Gly Ile Lys His
 185 190 195

gaa cga agc atg aaa aag gcc ctc gcg gtg tcc ttg ccg atg gca att 739
 Glu Arg Ser Met Lys Lys Ala Leu Ala Val Ser Leu Pro Met Ala Ile
 200 205 210

tgg gtg ttc agc tgc atc acc acc tcc ctg atc gtg atg tcc gcg cgc 787
 Trp Val Phe Ser Cys Ile Thr Thr Ser Leu Ile Val Met Ser Ala Arg
 215 220 225

atc gac tcc acc ttc ggc aac gcc att ctt ctc ccc gga atc ggc gcg 835
 Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu Leu Pro Gly Ile Gly Ala
 230 235 240 245

gcg atc gcc ttc agc gca ggc ctg atc gca caa ttt tta ggt agg aaa 883
 Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala Gln Phe Leu Gly Arg Lys
 250 255 260

ttc gcg tgg ggt cgt ggc tcc gga atc gtg ggc gcg ctg tgt gcc ctc 931
 Phe Ala Trp Gly Arg Gly Ser Gly Ile Val Gly Ala Leu Cys Ala Leu
 265 270 275

gcg ggt ttt gcg ctg gca gct ttt ggt ggc gac tcc att cca gtg tgg 979
 Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly Asp Ser Ile Pro Val Trp
 280 285 290

ctt ttc gtt atc gcc tcg atc ctg ttc ggc acc gca tat ggc ctc tgc 1027
 Leu Phe Val Ile Ala Ser Ile Leu Phe Gly Thr Ala Tyr Gly Leu Cys
 295 300 305

ctg cgc gaa ggc ctc ctc agc atc gaa act tac acg cca ctc aac cga 1075
 Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr Tyr Thr Pro Leu Asn Arg
 310 315 320 325

cgt ggc acc ggc atc ggc atc tat tat gtg ttc acg tat ttg gga ttc 1123
 Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val Phe Thr Tyr Leu Gly Phe
 330 335 340

ggg ctg cca gtg ctt ctc gac gcc ctc ctc ccg cac ctt ggc gcc tcc 1171
 Gly Leu Pro Val Leu Leu Asp Ala Leu Leu Pro His Leu Gly Ala Ser
 345 350 355

att ccg ctg tac gcg ctg gcg gcg ctc gcc ctt ggc tcc gca gta atc 1219

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Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala Leu Gly Ser Ala Val Ile
 360 365 370

cgc ggc gta caa atc aag cgc ggg tat gtg gtt tagatttcta cctacgacct 1272
 Arg Gly Val Gln Ile Lys Arg Gly Tyr Val Val
 375 380

gaa

1275

<210> 162

<211> 384

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 162

Met Arg Ser Gly Asn Ala Asn Arg Val Phe Ile Gly Val Thr Ile Leu
 1 5 10 15

Leu Phe Thr Ala Gly Trp Ala Ala Asn His Phe Ala Ser Val Leu Val
 20 25 30

Leu Ile Arg Glu Gln Leu Asp Val Ser Ser Val Leu Val Asn Gly Ala
 35 40 45

Phe Gly Ile Tyr Ala Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly Gly
 50 55 60

Val Leu Ala Asp Arg Phe Gly Ala Arg Met Val Val Leu Thr Gly Gly
 65 70 75 80

Val Leu Ser Ala Leu Gly Asn Leu Ser Leu Leu Ala Phe His Asp Gly
 85 90 95

Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly Leu
 100 105 110

Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala Ser
 115 120 125

Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met Gly
 130 135 140

Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile Thr
 145 150 155 160

Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val Gly
 165 170 175

Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala Ser
 180 185 190

Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val Ser
 195 200 205

Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu Ile
 210 215 220

Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu Leu
 225 230 235 240

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Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala Gln
245 250 255

Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val Gly
260 265 270

Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly Asp
275 280 285

Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly Thr
290 295 300

Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr Tyr
305 310 315 320

Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val Phe
325 330 335

Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu Pro
340 345 350

His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala Leu
355 360 365

Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val Val
370 375 380

<210> 163
 <211> 1130
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(1107)
 <223> FRXA01922

<400> 163
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 Leu Leu Phe Thr Ala Gly Trp Ala Ala Asn His Phe Ala Ser Val Leu
 1 5 10 15

gtg ttg atc cgt gaa caa tta gac gta tca agc gtg ctg gtc aac ggc 96
 Val Leu Ile Arg Glu Gln Leu Asp Val Ser Ser Val Leu Val Asn Gly
 20 25 30

gct ttt ggt att tat gca ctg gga ctt ctt cca agt ttg ctc gca ggc 144
 Ala Phe Gly Ile Tyr Ala Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly
 35 40 45

ggt gtg ctt gcc gac cgt ttt ggt gcc cgc atg gtg gta ctc acc gga 192
 Gly Val Leu Ala Asp Arg Phe Gly Ala Arg Met Val Val Leu Thr Gly
 50 55 60

ggt gta ctt tct gcg ctt gga aac ctt tct ctt tta gcg ttt cat gat 240
 Gly Val Leu Ser Ala Leu Gly Asn Leu Ser Leu Leu Ala Phe His Asp
 65 70 75 80

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ggt cct tcc ctc ctg gta gga cga ttc atc gtt ggt ctg ggc gtt gga 288
 Gly Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly
 85 90 95

tta gtc gtc agc gcg ggc acc gca tgg gcg ggc aga ttg cgc gga gca 336
 Leu Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala
 100 105 110

agc ggc gtg aca ttg gcc ggc att att ctg acc gcc ggt ttc atg atg 384
 Ser Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met
 115 120 125

ggg ccg att gtg aca agt ggg ttg ggg atg gcg tcg aca agc att att 432
 Gly Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile
 130 135 140

acg ccc ttt gcc ata agc gtt gcc ctc tcg ctg atc gcg gtg gtt gtg 480
 Thr Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val
 145 150 155 160

gga ttt gcg ctt ggc gat gcc cgc agc acc ccg agc gca ctt ggc gca 528
 Gly Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala
 165 170 175

tcc agc gga atc aaa cac gaa cga agc atg aaa aag gcc ctc gcg gtg 576
 Ser Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val
 180 185 190

tcc ttg ccg atg gca att tgg gtg ttc agc tgc atc acc acc tcc ctg 624
 Ser Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu
 195 200 205

atc gtg atg tcc gcg cgc atc gac tcc acc ttc ggc aac gcc att ott 672
 Ile Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu
 210 215 220

ctc ccc gga atc ggc gcg gcg atc gcc ttc agc gca ggc ctg atc gca 720
 Leu Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala
 225 230 235 240

caa ttt tta ggt agg aaa ttc gcg tgg ggt cgt ggc tcc gga atc gtg 768
 Gln Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val
 245 250 255

ggc gcg ctg tgt gcc ctc gcg ggt ttt gcg ctg gca gct ttt ggt ggc 816
 Gly Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly
 260 265 270

gac tcc att cca gtg tgg ctt ttc gtt atc gcc tcg atc ctg ttc ggc 864
 Asp Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly
 275 280 285

acc gca tat ggc ctc tgc ctg cgc gaa ggc ctc ctc agc atc gaa act 912
 Thr Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr
 290 295 300

tac acg cca ctc aac cga cgt ggc acc ggc atc ggc atc tat tat gtg 960
 Tyr Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val
 305 310 315 320

00603208-062300

ttc acg tat ttg gga ttc ggg ctg cca gtg ctt ctc gac gcc ctc ctc 1008
 Phe Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu
 325 330 335
 ccg cac ctt ggc gcc tcc att ccg ctg tac gcg ctg gcg gcg ctc gcc 1056
 Pro His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala
 340 345 350
 ctt ggc tcc gca gta atc cgc gcc gta caa atc aag cgc ggg tat gtg 1104
 Leu Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val
 355 360 365
 gtt tagatttcta cctacgacct gaa 1130
 Val

<210> 164
 <211> 369
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 164
 Leu Leu Phe Thr Ala Gly Trp Ala Ala Asn His Phe Ala Ser Val Leu
 1 5 10 15
 Val Leu Ile Arg Glu Gln Leu Asp Val Ser Ser Val Leu Val Asn Gly
 20 25 30
 Ala Phe Gly Ile Tyr Ala Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly
 35 40 45
 Gly Val Leu Ala Asp Arg Phe Gly Ala Arg Met Val Val Leu Thr Gly
 50 55 60
 Gly Val Leu Ser Ala Leu Gly Asn Leu Ser Leu Leu Ala Phe His Asp
 65 70 75 80
 Gly Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly
 85 90 95
 Leu Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala
 100 105 110
 Ser Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met
 115 120 125
 Gly Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile
 130 135 140
 Thr Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val
 145 150 155 160
 Gly Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala
 165 170 175
 Ser Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val
 180 185 190
 Ser Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu
 195 200 205

00663203.062300

Ile Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu
210 215 220

Leu Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala
225 230 235 240

Gln Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val
245 250 255

Gly Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly
260 265 270

Asp Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly
275 280 285

Thr Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr
290 295 300

Tyr Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val
305 310 315 320

Phe Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu
325 330 335

Pro His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala
340 345 350

Leu Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val
355 360 365

Val

<210> 165

<211> 362

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(339)

<223> RXA02060

<400> 165

gaa ttt gcc cgc att ttg aag cca aag gga cag gtc atc gtg ctt acc 48
Glu Phe Ala Arg Ile Leu Lys Pro Lys Gly Gln Val Ile Val Leu Thr
1 5 10 15

gca gat acc gcc cac ttg gct gag ctt cgt gaa cca ctg ggc atc att 96
Ala Asp Thr Gly His Leu Ala Glu Leu Arg Glu Pro Leu Gly Ile Ile
20 25 30

gat gtg gag gcc gcc aaa gtt gat cgc atg atc gaa caa gcg gca gcc 144
Asp Val Glu Ala Gly Lys Val Asp Arg Met Ile Glu Gln Ala Ala Gly
35 40 45

cac ctc aag cca gtt gcc gaa aga gac ttg gtg gaa ttt gaa atg ctg 192
His Leu Lys Pro Val Gly Glu Arg Asp Leu Val Glu Phe Glu Met Leu
50 55 60

00603208.062300

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ctg gat caa aaa tcc att gca tct cag atc ggt atg agc cct tct gca 240
Leu Asp Gln Lys Ser Ile Ala Ser Gln Ile Gly Met Ser Pro Ser Ala
65 70 75 80

cgc cac att aag cct gag gct ttg gcg gaa cgc atc gcc gct cta cca 288
Arg His Ile Lys Pro Glu Ala Leu Ala Glu Arg Ile Ala Ala Leu Pro
85 90 95

gaa caa atg aag gtt aca gcc cgg gcc aag atc acc agg ctg gaa cgc 336
Glu Gln Met Lys Val Thr Ala Arg Ala Lys Ile Thr Arg Leu Glu Arg
100 105 110

atc taactcttat ctcactgggc ctt 362
Ile

```

```

<210> 166
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

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<400> 166
Glu Phe Ala Arg Ile Leu Lys Pro Lys Gly Gln Val Ile Val Leu Thr
1 5 10 15

Ala Asp Thr Gly His Leu Ala Glu Leu Arg Glu Pro Leu Gly Ile Ile
20 25 30

Asp Val Glu Ala Gly Lys Val Asp Arg Met Ile Glu Gln Ala Ala Gly
35 40 45

His Leu Lys Pro Val Gly Glu Arg Asp Leu Val Glu Phe Glu Met Leu
50 55 60

Leu Asp Gln Lys Ser Ile Ala Ser Gln Ile Gly Met Ser Pro Ser Ala
65 70 75 80

Arg His Ile Lys Pro Glu Ala Leu Ala Glu Arg Ile Ala Ala Leu Pro
85 90 95

Glu Gln Met Lys Val Thr Ala Arg Ala Lys Ile Thr Arg Leu Glu Arg
100 105 110

Ile

```

```

<210> 167
<211> 1395
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1372)
<223> RXN01936

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<400> 167
gcgcggtgac accacagccg ttgtcagcgg cgcttggtct gtggaggatc gccgaggtta 60

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00603208.062300

ctaacaataa	ggcccaacaa	agaggtctaa	gctctacctg	gtg	agt	ttc	cga	gat	115
				Val	Ser	Phe	Arg	Asp	
				1				5	
att ttc gct gac acc aga ccg ctg aaa gaa ccg gcc ttc aaa cgc ctc	163								
Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro Ala Phe Lys Arg Leu									
	10								
	15								
tgg ctt ggc aat gtt gcc acc gtc att ggt gcc caa tta act gtt gtt	211								
Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala Gln Leu Thr Val Val									
	25								
	30								
	35								
gcc gtt ccg gtg cag att tac caa atg act ggg tcc tcc gcc tat gtg	259								
Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly Ser Ser Gly Tyr Val									
	40								
	45								
	50								
ggc ttg acc ggg ctt ttt ggc ctt att cct ttg gtt att ttt ggc ctt	307								
Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu Val Ile Phe Gly Leu									
	55								
	60								
tat ggt gga tcc att gcg gat gct ttt gat aaa cgc atc gtg ctg atc	355								
Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys Arg Ile Val Leu Ile									
	70								
	75								
	80								
	85								
tgc acc acg atc ggc atg tgt gtc acc act gcc ggt ttt tgg gtg ctg	403								
Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala Gly Phe Trp Val Leu									
	90								
	95								
	100								
acc att tta ggc aat gag aat att tgg ctc ctg tta ata aac ttt tct	451								
Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu Leu Ile Asn Phe Ser									
	105								
	110								
	115								
tta cag cag gca ttt ttc gcg gtg aat caa ccc acc cga acg gcg atc	499								
Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro Thr Arg Thr Ala Ile									
	120								
	125								
	130								
ctt cga agt att ttg ccg att gat caa tta gcg tgg gca aca tca ctg	547								
Leu Arg Ser Ile Leu Pro Ile Asp Gln Leu Ala Ser Ala Thr Ser Leu									
	135								
	140								
	145								
aat atg ctg ctc atg cag acc ggc gca atc gtt gcc ccg ctg atc gca	595								
Asn Met Leu Leu Met Gln Thr Gly Ala Ile Val Gly Pro Leu Ile Ala									
	150								
	155								
	160								
	165								
ggt gcg ttg att ccg ctg atc ggt ttc ggg tgg ctg tat ttc ctt gat	643								
Gly Ala Leu Ile Pro Leu Ile Gly Phe Trp Leu Tyr Phe Leu Asp									
	170								
	175								
	180								
gtt gtc tcc atc atc ccc aca ctg tgg gct gta tgg tca ctg cct tcg	691								
Val Val Ser Ile Ile Pro Thr Leu Trp Trp Ala Val Trp Ser Leu Pro Ser									
	185								
	190								
	195								
atc aag cca tcc ggc aag gtg atg aag gct ggt ttc gcc agt gtg gtg	739								
Ile Lys Pro Ser Gly Lys Val Met Lys Ala Gly Phe Ala Ser Val Val									
	200								
	205								
	210								
gat ggc ctg aag tat ttg gct ggc caa ccc gtg ttg ttg atg gtg atg	787								
Asp Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val Leu Leu Met Val Met									
	215								
	220								
	225								

09036

[illegible]

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<210> 168
<211> 424
<212> PRT
<213> Corynebacterium glutamicum
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<400> 168
Val Ser Phe Arg Asp Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro
  1           5           10           15
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Ala Phe Lys Arg Leu Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala
 20 25 30
 Gln Leu Thr Val Val Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly
 35 40 45
 Ser Ser Gly Tyr Val Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu
 50 55 60
 Val Ile Phe Gly Leu Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys
 65 70 75 80
 Arg Ile Val Leu Ile Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala
 85 90 95
 Gly Phe Trp Val Leu Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu
 100 105 110
 Leu Ile Asn Phe Ser Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro
 115 120 125
 Thr Arg Thr Ala Ile Leu Arg Ser Ile Leu Pro Ile Asp Gln Leu Ala
 130 135 140
 Ser Ala Thr Ser Leu Asn Met Leu Leu Met Gln Thr Gly Ala Ile Val
 145 150 155 160
 Gly Pro Leu Ile Ala Gly Ala Leu Ile Pro Leu Ile Gly Phe Gly Trp
 165 170 175
 Leu Tyr Phe Leu Asp Val Val Ser Ile Ile Pro Thr Leu Trp Ala Val
 180 185 190
 Trp Ser Leu Pro Ser Ile Lys Pro Ser Gly Lys Val Met Lys Ala Gly
 195 200 205
 Phe Ala Ser Val Val Asp Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val
 210 215 220
 Leu Leu Met Val Met Val Leu Asp Leu Ile Ala Met Ile Phe Gly Met
 225 230 235 240
 Pro Arg Ala Leu Tyr Pro Glu Ile Ala Glu Val Asn Phe Gly Gly Gly
 245 250 255
 Asp Ala Gly Ala Thr Met Leu Ala Phe Met Tyr Ser Ser Met Ala Val
 260 265 270
 Gly Ala Val Leu Gly Gly Val Leu Ser Gly Trp Val Ala Arg Ile Ser
 275 280 285
 Arg Gln Gly Val Ala Val Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala
 290 295 300
 Val Ala Leu Gly Gly Val Ala Ile Val Val Ser Pro Gly Ala Val Thr
 305 310 315 320
 Ala Trp Ala Trp Met Phe Ile Ile Met Met Val Ile Gly Gly Met Ala
 325 330 335

00503208-062300

Asp Met Phe Ser Ser Ala Val Arg Asn Ala Ile Leu Gln Gln Ser Ala
 340 345 350
 Ala Glu His Val Gln Gly Arg Ile Gln Gly Val Trp Ile Ile Val Val
 355 360
 Val Gly Gly Pro Arg Leu Ala Asp Val Leu His Gly Trp Ala Ala Glu
 370 375 380
 Pro Leu Gly Ala Gly Trp Thr Val Leu Trp Gly Gly Val Ala Val Val
 385 390 395 400
 Val Leu Thr Ala Ile Cys Met Val Ala Val Pro Lys Phe Trp Lys Tyr
 405 410 415
 Glu Lys Pro Lys Ile Thr Gly Ile
 420

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<210> 169
<211> 945
<212> DNA
<213> Corvnebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(922)
<223> FRXA01936
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4400> 169	tttacagcag gcatTTTTcg cggtgaatca accaccCGa acgGcgatcc ttcgaagtat	60
	tttgCGcatt gatcaataag cgtCGgcaac atcaCTgaat	115
	Met 1 Leu 5 Leu 5 Met 5 Gln 5	
	acc ggc gca atc gtt ggc cgc ctg atc gca ggt gcg ttg att ccg ctg	163
	Thr Gly Ala Ile Val Gly Pro Leu Ile Ala Gly Ala Leu Ile Pro Leu	
	10 15 20	
	atc ggt ttc ggg tgg ctg tat ttc ctt gat gtt gtc tcc atc atc ccc	211
	Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp Val Val Ser Ile Ile Pro	
	25 30 35	
	aca ctg tgg gct gta tgg tca ctg cct tcg atc aag cca tcc ggc aag	259
	Thr Leu Trp Ala Val Trp Ser Leu Pro Ser Ile Lys Pro Ser Gly Lys	
	40 45 50	
	gtg atg aag gct ggt ttc gcc agt gtg gtg gat ggc ctg aag tat ttg	307
	Val Met Lys Ala Gly Phe Ala Ser Val Val Asp Gly Leu Lys Tyr Leu	
	55 60 65	
	gct ggc caa ccc gtg ttg ttg atg gtg atg gtg ctg gat ctt atc gcc	355
	Ala Gly Gln Pro Val Leu Leu Met Val Met Val Leu Asp Leu Ile Ala	
	70 75 80 85	
	atg att ttc ggc atg cca cgt gcg ctt tac ccc gag atc gca gaa gtg	403
	Met Ile Phe Gly Met Pro Arg Ala Leu Tyr Pro Glu Ile Ala Glu Val	
	90 95 100	
	aac ttc ggt ggg ggt gac gcc ggt gca acg atg ctg gcg ttc atg tac	451

DEFECTION

Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr Met Leu Ala Phe Met Tyr
 105 110 115
 tca tcc atg gct gtt ggc gca gtt ctt ggc ggc gtg ctg tct ggt tgg 499
 Ser Ser Met Ala Val Gly Ala Val Leu Gly Gly Val Leu Ser Gly Trp
 120 125 130
 gtg gcc cgg att agc cgc cag ggt gtt gca gtt tat tgg tgc atc atc 547
 Val Ala Arg Ile Ser Arg Gln Gly Val Ala Val Tyr Trp Cys Ile Ile
 135 140 145
 gcc tgg ggc gca gcc gtt gct ttg ggt ggt gtg gca att gtt gtc agc 595
 Ala Trp Gly Ala Ala Val Ala Leu Gly Gly Val Ala Ile Val Val Ser
 150 155 160 165
 ccc ggc gcg gtg act gcg tgg gcg tgg atg ttc atc atc atg atg gtc 643
 Pro Gly Ala Val Thr Ala Trp Ala Trp Met Phe Ile Ile Met Met Val
 170 175 180
 att ggt ggc atg gct gac atg ttc agc tcg gca gtt cga aac gct att 691
 Ile Gly Gly Met Ala Asp Met Phe Ser Ser Ala Val Arg Asn Ala Ile
 185 190 195
 ttg cag cag tct gct gcg gaa cat gtg cag ggc cga atc caa ggt gtg 739
 Leu Gln Gln Ser Ala Ala Glu His Val Gln Gly Arg Ile Gln Gly Val
 200 205 210
 tgg atc atc gtc gtg gtg ggt gga cct cgt tta gct gac gtc ctt cac 787
 Trp Ile Ile Val Val Val Gly Gly Pro Arg Leu Ala Asp Val Leu His
 215 220 225
 ggt tgg gcc gct gag ccc ctc gcc gca ggt tgg acg gta tta tgg gcc 835
 Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly Trp Thr Val Leu Trp Gly
 230 235 240 245
 gga gta gcg gtg gtt gta ctc act gca att tgt atg gtg gcg gtg cct 883
 Gly Val Ala Val Val Val Leu Thr Ala Ile Cys Met Val Ala Val Pro
 250 255 260
 aaa ttc tgg aaa tac gag aaa cca aaa att acc gcc atc taaatactta 932
 Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile Thr Gly Ile
 265 270
 tccatgccca ttt 945

 <210> 170
 <211> 274
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 170
 Met Leu Leu Met Gln Thr Gly Ala Ile Val Gly Pro Leu Ile Ala Gly
 1 5 10 15
 Ala Leu Ile Pro Leu Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp Val
 20 25 30
 Val Ser Ile Ile Pro Thr Leu Trp Ala Val Trp Ser Leu Pro Ser Ile
 35 40 45

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Lys Pro Ser Gly Lys Val Met Lys Ala Gly Phe Ala Ser Val Val Asp
 50 55 60
 Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val Leu Leu Met Val Met Val
 65 70 75 80
 Leu Asp Leu Ile Ala Met Ile Phe Gly Met Pro Arg Ala Leu Tyr Pro
 85 90 95
 Glu Ile Ala Glu Val Asn Phe Gly Gly Asp Ala Gly Ala Thr Met
 100 105 110
 Leu Ala Phe Met Tyr Ser Ser Met Ala Val Gly Ala Val Leu Gly Gly
 115 120 125
 Val Leu Ser Gly Trp Val Ala Arg Ile Ser Arg Gln Gly Val Ala Val
 130 135 140
 Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala Val Ala Leu Gly Gly Val
 145 150 155 160
 Ala Ile Val Val Ser Pro Gly Ala Val Thr Ala Trp Ala Trp Met Phe
 165 170 175
 Ile Ile Met Met Val Ile Gly Gly Met Ala Asp Met Phe Ser Ser Ala
 180 185 190
 Val Arg Asn Ala Ile Leu Gln Gln Ser Ala Ala Glu His Val Gln Gly
 195 200 205
 Arg Ile Gln Gly Val Trp Ile Ile Val Val Val Gly Gly Pro Arg Leu
 210 215 220
 Ala Asp Val Leu His Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly Trp
 225 230 235 240
 Thr Val Leu Trp Gly Gly Val Ala Val Val Val Leu Thr Ala Ile Cys
 245 250 255
 Met Val Ala Val Pro Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile Thr
 260 265 270
 Gly Ile

<210> 171
 <211> 549
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(526)
 <223> FRXA01937

<400> 171
 gcgcggtgac accacagccg ttgtcagcgg cgcttggtct gtggaggatc gccgaggtta 60
 ctaacaaata ggcccaacaa agaggtctaa gctctacctg gtg agt ttc cga gat 115
 Val Ser Phe Arg Asp

002290.002300

															1					5
att	ttc	gct	gac	acc	aga	ccg	ctg	aaa	gaa	ccg	gcc	ttc	aaa	cgc	ctc	163				
Ile	Phe	Ala	Asp	Thr	Arg	Pro	Leu	Lys	Glu	Pro	Ala	Phe	Lys	Arg	Leu					
				10					15					20						
tgg	ctt	ggc	aat	gtt	gcc	acc	gtc	att	ggg	gcc	caa	tta	act	gtt	gtt	211				
Trp	Leu	Gly	Asn	Val	Ala	Thr	Val	Ile	Gly	Ala	Gln	Leu	Thr	Val	Val					
				25					30					35						
gcc	gtt	ccg	gtg	cag	att	tac	caa	atg	act	ggg	tcc	tcc	ggc	tat	gtg	259				
Ala	Val	Pro	Val	Gln	Ile	Tyr	Gln	Met	Thr	Gly	Ser	Ser	Gly	Tyr	Val					
				40					45					50						
ggc	ttg	acc	ggg	ctt	ttt	ggc	ctt	att	cct	ttg	gtt	att	ttt	ggc	ctt	307				
Gly	Leu	Thr	Gly	Leu	Phe	Gly	Leu	Ile	Pro	Leu	Val	Ile	Phe	Gly	Leu					
				55					60					65						
tat	ggg	gga	tcc	att	gcg	gat	gct	ttt	gat	aaa	cgc	atc	gtg	ctg	atc	355				
Tyr	Gly	Gly	Ser	Ile	Ala	Asp	Ala	Phe	Asp	Lys	Arg	Ile	Val	Leu	Ile					
				70					75					80	85					
tgc	acc	acg	atc	ggc	atg	tgt	gtc	acc	act	gcc	ggt	ttt	tgg	gtg	ctg	403				
Cys	Thr	Thr	Ile	Gly	Met	Cys	Val	Thr	Thr	Ala	Gly	Phe	Trp	Val	Leu					
				90					95					100						
acc	att	tta	ggc	aat	gag	aat	att	tgg	ctc	ctg	tta	ata	aac	ttt	tct	451				
Thr	Ile	Leu	Gly	Asn	Glu	Asn	Ile	Trp	Leu	Leu	Leu	Ile	Asn	Phe	Ser					
				105					110					115						
tta	cag	cag	gca	ttt	ttc	gcg	gtg	aat	caa	ccc	acc	cga	acg	gcg	atc	499				
Leu	Gln	Gln	Ala	Phe	Phe	Ala	Val	Asn	Gln	Pro	Thr	Arg	Thr	Ala	Ile					
				120					125					130						
ctt	cga	agt	att	ttg	ccg	att	gat	caa	taagcgtcgg	caacatcact						546				
Leu	Arg	Ser	Ile	Leu	Pro	Ile	Asp	Gln												
				135					140											
gaa															549					

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<210> 172
<211> 142
<212> PRT
<213> Corynebacterium glutamicum
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400> 172
Val Ser Phe Arg Asp Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro
  1          5          10          15          20
Ala Phe Lys Arg Leu Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala
          20          25          30          35          40
Gln Leu Thr Val Val Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly
          35          40          45          50          55
Ser Ser Gly Tyr Val Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu
          50          55          60          65          70
Val Ile Phe Gly Leu Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys
  65          70          75          80          85

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Arg	Ile	Val	Leu	Ile	Cys	Thr	Thr	Ile	Gly	Met	Cys	Val	Thr	Thr	Ala
				85					90					95	
Gly	Phe	Trp	Val	Leu	Thr	Ile	Leu	Gly	Asn	Glu	Asn	Ile	Trp	Leu	Leu
			100					105					110		
Leu	Ile	Asn	Phe	Ser	Leu	Gln	Gln	Ala	Phe	Phe	Ala	Val	Asn	Gln	Pro
		115					120					125			
Thr	Arg	Thr	Ala	Ile	Leu	Arg	Ser	Ile	Leu	Pro	Ile	Asp	Gln		
	130					135					140				

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<210> 173
<211> 1242
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1219)
<223> RXN01010
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400> 173																		
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aaaagatctg	gcaggggggtt	tagggcataga	ttaggaactt	atg	aag	aaa	ctg	caa									115	
				Met	Lys	Lys	Leu	Gln										
				1														
atg	ccg	gcc	att	ttg	gtc	gga	ggc	ttt	gtg	ggg	ccg	ttt	act	ggc	caa	163		
Met	Pro	Ala	Ile	Leu	Val	Gly	Gly	Phe	Val	Gly	Pro	Phe	Thr	Gly	Gln			
				10					15					20				
gct	cta	tca	gtg	gtc	ttg	ccg	gaa	ttt	gca	gac	acc	ttt	gat	atc	agt	211		
Ala	Leu	Ser	Val	Val	Leu	Pro	Glu	Phe	Ala	Asp	Thr	Phe	Asp	Ile	Ser			
			25					30					35					
gtc	agc	cag	gca	gcg	ctg	acc	atg	acc	gca	tac	ttg	ttg	ccc	ttt	gcc	259		
Val	Ser	Gln	Ala	Ala	Leu	Thr	Met	Thr	Ala	Tyr	Leu	Leu	Pro	Phe	Ala			
			40				45					50						
acc	atg	atg	ttg	ttt	tgg	ggg	cgc	atc	acc	aga	aag	atc	cat	ccg	cat	307		
Thr	Met	Met	Leu	Phe	Ser	Gly	Arg	Ile	Thr	Arg	Lys	Ile	His	Pro	His			
			55			60					65							
aag	gtg	gtg	cag	gcg	gct	tat	att	gtc	aca	ctg	cca	ctt	gcg	ctg	ttg	355		
Lys	Val	Val	Gln	Ala	Ala	Tyr	Ile	Val	Thr	Leu	Pro	Leu	Ala	Leu	Leu			
	70				75					80				85				
ctc	cta	gtt	aca	cca	tgg	tgg	ggg	ctg	ttt	atg	gct	gcg	tat	gcc	acg	403		
Leu	Leu	Val	Thr	Pro	Ser	Trp	Gly	Leu	Phe	Met	Ala	Ala	Tyr	Ala	Thr			
			90					95						100				
att	ggg	atc	gct	aas	gca	ttt	acc	act	ccg	gtg	ctg	caa	att	atg	ttg	451		
Ile	Gly	Ile	Ala	Asn	Ala	Phe	Thr	Thr	Pro	Val	Leu	Gln	Ile	Met	Leu			
			105					110					115					
cgt	gag	ctt	gtt	ccg	ccg	cgt	tct	ttg	ggt	aag	gca	ttg	ggc	acc	tat	499		
Arg	Glu	Leu	Val	Pro	Pro	Arg	Ser	Gly	Gly	Lys	Ala	Leu	Gly	Thr	Tyr			

120	125	130	
gct gcg atg caa tca ctc ggc atg ttg tcg gcg cca ctg atc gca ggt Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala Pro Leu Ile Ala Gly 135 140 145			547
gtg tct tcg gtg gtg tcg tgg agg ttg acc ttc ctg gtc act gca gca Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe Leu Val Thr Ala Ala 150 155 160 165			595
gcg tca ctg ttt att ttg gtg gcg cga ctc ccc gtt gtt cca cca cca Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro Val Val Pro Pro Pro 170 175 180			643
tca gca tcg aag caa aac gtt agt ggc aag gtg cag tgg gga ccg acc Ser Ala Ser Lys Gln Asn Val Ser Gly Lys Val Gln Trp Gly Pro Thr 185 190 195			691
atc atc cac atg gtt tcc ggc ttt gtg gtg ggc atc ggc atc atc ggc Ile Ile His Met Val Ser Gly Phe Val Val Gly Ile Gly Ile Ile Gly 200 205 210			739
att gga ttc atg aca tcg ctg cac gtt ggc gag caa ttc gga ctt gat Ile Gly Phe Met Thr Ser Leu His Val Gly Glu Gln Phe Gly Leu Asp 215 220 225			787
gct gca gcg cgt ggt ttg gtg gtc atg tgt ggt ggc ctg gct gcg ttc Ala Ala Ala Arg Gly Leu Val Val Met Cys Gly Gly Leu Ala Ala Phe 230 235 240 245			835
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gcg gtg ctc att gtc agt gct gtc atc ggt acc atc gca ctc gca ctg Ala Val Leu Ile Val Ser Ala Val Ile Gly Thr Ile Ala Leu Ala Leu 265 270 275			931
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gca gta gca gca gca caa gga atc caa gca acc gtc aac ttg gct gtc Ala Val Ala Ala Ala Gln Gly Ile Gln Ala Thr Val Asn Leu Ala Val 295 300 305			1027
atc gga agc ccc ggt gga tca tcg ctg ctt tct acc gtg cag gct ttc Ile Gly Ser Pro Gly Gly Ser Ser Leu Leu Ser Thr Val Gln Ala Phe 310 315 320 325			1075
cga ttc ttc gga tca gcg gca gca cca gtg aca ttc ctt cct atc tat Arg Phe Phe Gly Ser Ala Ala Ala Pro Val Thr Phe Leu Pro Ile Tyr 330 335 340			1123
atg ggc atc ggc tcg ggg gcg ttt tgg gtc agc gcg gta gcg ctg ttc Met Gly Ile Gly Ser Gly Ala Phe Trp Val Ser Ala Val Ala Leu Phe 345 350 355			1171
ttc gtt gcc atc gcc cag tgg ctc aac ccg cag cgg gtg gag cgg ggc Phe Val Ala Ile Ala Gln Trp Leu Asn Pro Gln Arg Val Glu Arg Gly 360 365 370			1219

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1242

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<213> Corynebacterium glutamicum

<400> 174

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Thr Phe Asp Ile Ser Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr
 35 40 45

Leu Leu Pro Phe Ala Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg
 50 55 60

Lys Ile His Pro His Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu
 65 70 75 80

Pro Leu Ala Leu Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met
 85 90 95

Ala Ala Tyr Ala Thr Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val
 100 105 110

Leu Gln Ile Met Leu Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys
 115 120 125

Ala Leu Gly Thr Tyr Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala
 130 135 140

Pro Leu Ile Ala Gly Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe
 145 150 155 160

Leu Val Thr Ala Ala Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro
 165 170 175

Val Val Pro Pro Pro Ser Ala Ser Lys Gln Asn Val Ser Gly Lys Val
 180 185 190

Gln Trp Gly Pro Thr Ile Ile His Met Val Ser Gly Phe Val Val Gly
 195 200 205

Ile Gly Ile Ile Gly Ile Gly Phe Met Thr Ser Leu His Val Gly Glu
 210 215 220

Gln Phe Gly Leu Asp Ala Ala Ala Arg Gly Leu Val Val Met Cys Gly
 225 230 235 240

Gly Leu Ala Ala Phe Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp
 245 250 255

Lys Phe Gly Val Arg Ala Val Leu Ile Val Ser Ala Val Ile Gly Thr
 260 265 270

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 Val Leu Trp Ala Phe Ala Val Ala Ala Ala Gln Gly Ile Gln Ala Thr
 290 295 300
 Val Asn Leu Ala Val Ile Gly Ser Pro Gly Gly Ser Ser Leu Leu Ser
 305 310 315 320
 Thr Val Gln Ala Phe Arg Phe Phe Gly Ser Ala Ala Ala Pro Val Thr
 325 330 335
 Phe Leu Pro Ile Tyr Met Gly Ile Gly Ser Gly Ala Phe Trp Val Ser
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 Arg Val Glu Arg Gly
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 <213> Corynebacterium glutamicum

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 <223> FRXA01010

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 Met Lys Lys Leu Gln
 1 5
 atg ccg gcc att ttg gtc gga ggc ttt gtg ggg ccg ttt act ggc caa 163
 Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly Pro Phe Thr Gly Gln
 10 15 20
 gct cta tca gtg gtc ttg ccg gaa ttt gca gac acc ttt gat atc agt 211
 Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp Thr Phe Asp Ile Ser
 25 30 35
 gtc agc cag gca gcg ctg acc atg acc gca tac ttg ttg ccc ttt gcc 259
 Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr Leu Leu Pro Phe Ala
 40 45 50
 acc atg atg ttg ttt tcg ggg cgc atc acc aga aag atc cat ccg cat 307
 Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg Lys Ile His Pro His
 55 60 65
 aag gtg gtg cag gcg gct tat att gtc aca ctg cca ctt gcg ctg ttg 355
 Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu Pro Leu Ala Leu Leu
 70 75 80 85
 ctc cta gtt aca cca tcg tgg ggg ctg ttt atg gct gcg tat gcc acg 403
 Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met Ala Ala Tyr Ala Thr

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 Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val Leu Gln Ile Met Leu
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 cgt gag ett gtt ccg ccg cgt tct ttg ggt aag gca ttg ggc acc tat 499
 Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys Ala Leu Gly Thr Tyr
 120 125 130
 gct gcg atg caa tca ctc ggc atg ttg tcg gcg cca ctg atc gca ggt 547
 Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala Pro Leu Ile Ala Gly
 135 140 145
 gtg tct tcg gtg gtg tcg tgg agg ttg acc ttc ctg gtc act gca gca 595
 Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe Leu Val Thr Ala Ala
 150 155 160 165
 gcg tca ctg ttt att ttg gtg gcg cga ctc ccc gtt gtt cca cca cca 643
 Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro Val Val Pro Pro Pro
 170 175 180
 tca gca ttg aag caa aac gtt agt ggc aag gtg cag tgg gga ccg acc 691
 Ser Ala Leu Lys Gln Asn Val Ser Gly Lys Val Gln Trp Gly Pro Thr
 185 190 195
 atc atc cac atg gtt tcc ggc ttt gtg gtg ggc atc ggc atc atc ggc 739
 Ile Ile His Met Val Ser Gly Phe Val Val Gly Ile Gly Ile Ile Gly
 200 205 210
 att gga ttc atg aca tcg ctg cac gtt ggc gag caa ttc gga ctt aat 787
 Ile Gly Phe Met Thr Ser Leu His Val Gly Glu Gln Phe Gly Leu Asn
 215 220 225
 act gca gcg cgt ggt ttg gtg gtc atg tgt ggt ggc cgg gct gcg ttc 835
 Thr Ala Ala Arg Gly Leu Val Val Met Cys Gly Gly Arg Ala Ala Phe
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 Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp Lys
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 Thr Phe Asp Ile Ser Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr
 35 40 45
 Leu Leu Pro Phe Ala Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg
 50 55 60

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Lys Ile His Pro His Lys Val Val Gln Ala Tyr Ile Val Thr Leu
 65 70 75 80
 Pro Leu Ala Leu Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met
 85 90 95
 Ala Ala Tyr Ala Thr Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val
 100 105 110
 Leu Gln Ile Met Leu Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys
 115 120 125
 Ala Leu Gly Thr Tyr Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala
 130 135 140
 Pro Leu Ile Ala Gly Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe
 145 150 155 160
 Leu Val Thr Ala Ala Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro
 165 170 175
 Val Val Pro Pro Pro Ser Ala Leu Lys Gln Asn Val Ser Gly Lys Val
 180 185 190
 Gln Trp Gly Pro Thr Ile Ile His Met Val Ser Gly Phe Val Val Gly
 195 200 205
 Ile Gly Ile Ile Gly Ile Gly Phe Met Thr Ser Leu His Val Gly Glu
 210 215 220
 Gln Phe Gly Leu Asn Thr Ala Ala Arg Gly Leu Val Val Met Cys Gly
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 Lys

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 <223> RXN03142

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 Val Phe Ile Leu Gly
 1 5

tgg ctc gtc aac ttg acc cag tac ttg agc ttc tac ttc ctg atc aca 163
 Trp Leu Val Asn Leu Thr Gln Tyr Leu Ser Phe Tyr Phe Leu Ile Thr
 10 15 20

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gtc atg gcg ctg tat gcg atg gaa agc ttc gcc gtt tca gag gcc gct 211
 Val Met Ala Leu Tyr Ala Met Glu Ser Phe Ala Val Ser Glu Ala Ala
 25 30 35

gtc gga ttt gcg gcc agc tcc ttt gtt atc ggc gca acc gtg gct cgt 259
 Val Gly Phe Ala Ala Ser Ser Phe Val Ile Gly Ala Thr Val Ala Arg
 40 45 50

gtg ttc gcg gga tgg acg tcc gac cgt ttt ggt aaa aaa cag atc ctg 307
 Val Phe Ala Gly Trp Thr Ser Asp Arg Phe Gly Lys Lys Gln Ile Leu
 55 60 65

ctc atc ttt gtc gcc ttg gaa gcg gta gca tca cta ttc tat att cca 355
 Leu Ile Phe Val Gly Leu Glu Ala Val Ala Ser Leu Phe Tyr Ile Pro
 70 75 80 85

gct gcc tca cta cca gcg ctg gtt gct gtg cgt ttt gtt cac ggt ttt 403
 Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg Phe Val His Gly Phe
 90 95 100

tct tat tct ctt gct tcc acc gct gtg atg gca ctt gtg cag tcc gtg 451
 Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala Leu Val His Ser Val
 105 110 115

att cct gca agc cgt agg gca gag gcc acc gcc tac ttc gcg ctc gga 499
 Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu Gly
 120 125 130

tcc aca ctg gct aca gct ttc gcc cca gca att gcg ctg ttt gtt atc 547
 Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile Ala Leu Phe Val Ile
 135 140 145

gat gac ttc aac tac aac acc ctg ttc tgg att acc act gcg acc agt 595
 Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr Ser
 150 155 160 165

gtt ttc gcc ctg atc ctc acc gtt ttg atc cgc aag ccg gag ttc att 643
 Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe Ile
 170 175 180

aag aat gcg gaa cac gcc aga gta aag cca gtc tgg tct atc aag act 691
 Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys Thr
 185 190 195

gtt gtg cac cca tcg gtc atg ctc att gga ttc ttc atg ctc gct gtc 739
 Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala Val
 200 205 210

gga ctg gct tac gca gcc gtg atc acc ttc ctc aac gcc ttc gcg caa 787
 Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala Gln
 215 220 225

gac act gcc ctc acc gcc gga gcg ggt ctt ttc ttt atc gct tat gcg 835
 Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala
 230 235 240 245

gtt gcg atg ctg gtc atg cgt ttc ttc ctt gga cgc att cag gac aaa 883
 Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp Lys
 250 255 260

cat ggt gac aac ccg gtt att tac ttc ggt ttg atc agc ttc gcc ctc 931

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His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala Leu
 265 270 275
 gcg ctg ggg ctt atg gct ttg gcg act gaa gac tgg cac att gtt ctc 979
 Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val Leu
 280 285 290
 gct ggc gca ctc acc ggt ttg ggc tat ggc acc atc atg cgg gcc gca 1027
 Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala Ala
 295 300 305
 caa gcc att gct gtc gat tca gtt cca agc act cag gtt ggt tcc ggt 1075
 Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser Gly
 310 315 320 325
 att tct acg ctt ttc ctg ttc acc gac atc ggc att ggc tta ggc cca 1123
 Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly Pro
 330 335 340
 atc ctg ctg ggt gga ttg gtt gca gcg acc gga tac aac gtc atg tac 1171
 Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met Tyr
 345 350 355
 gca gct ttg gcc gca gtg att gtt gtg gcg ggc gtg ctc tac ctg gtt 1219
 Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu Val
 360 365 370
 gct ttg ggt agg aaa gct agc cac taagtttagag cattttattg agc 1266
 Ala Leu Gly Arg Lys Ala Ser His
 375 380
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 <212> PRT
 <213> *Corynebacterium glutamicum*
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 Val Ser Glu Ala Ala Val Gly Phe Ala Ala Ser Ser Phe Val Ile Gly
 35 40 45
 Ala Thr Val Ala Arg Val Phe Ala Gly Trp Thr Ser Asp Arg Phe Gly
 50 55 60
 Lys Lys Gln Ile Leu Leu Ile Phe Val Gly Leu Glu Ala Val Ala Ser
 65 70 75 80
 Leu Phe Tyr Ile Pro Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg
 85 90 95
 Phe Val His Gly Phe Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala
 100 105 110
 Leu Val Gln Ser Val Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly
 115 120 125

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Tyr Phe Ala Leu Gly Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile
   130                               135                               140

Ala Leu Phe Val Ile Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile
  145                               150                               155                               160

Thr Thr Ala Thr Ser Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg
                               165                               170                               175

Lys Pro Glu Phe Ile Lys Asn Ala Glu His Gly Arg Val Lys Pro Val
                               180                               185                               190

Trp Ser Ile Lys Thr Val Val His Pro Ser Val Met Leu Ile Gly Phe
   195                               200                               205

Phe Met Leu Ala Val Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu
   210                               215                               220

Asn Gly Phe Ala Gln Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe
  225                               230                               235                               240

Phe Ile Ala Tyr Ala Val Ala Met Leu Val Met Arg Phe Phe Leu Gly
   245                               250                               255

Arg Ile Gln Asp Lys His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu
   260                               265                               270

Ile Ser Phe Ala Leu Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp
   275                               280                               285

Trp His Ile Val Leu Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr
   290                               295                               300

Ile Met Pro Ala Ala Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr
  305                               310                               315                               320

Gln Val Gly Ser Gly Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly
   325                               330                               335

Ile Gly Leu Gly Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly
   340                               345                               350

Tyr Asn Val Met Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly
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Val Leu Tyr Leu Val Ala Leu Gly Arg Lys Ala Ser His
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<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (1)..(891)

<223> FRXA01150

<400> 179

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 Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met
 260 265 270
 tac gca gct ttg gcc gca gtg att gtt gtg gcg ggc gtg ctc tac ctg 864
 Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu
 275 280 285
 gtt gct ttg ggt agg aaa gct agc cac taagtttagag cattttattg 911
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 290 295
 agc 914

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 Gly Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile Ala Leu Phe Val
 50 55 60
 Ile Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr
 65 70 75 80
 Ser Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe
 85 90 95
 Ile Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys
 100 105 110
 Thr Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala
 115 120 125
 Val Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala
 130 135 140
 Gln Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr
 145 150 155 160
 Ala Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp
 165 170 175
 Lys His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala
 180 185 190
 Leu Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val

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<213> Corynebacterium glutamicum

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<223> RXN02964

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                                     Val Ser Val Ala Glu
                                     1 5

gaa ggg aaa ctt ttt aca cca acg ttt gtc atg gga tgg ttt gcc aac 163
Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met Gly Trp Phe Ala Asn
                                     10 15 20

ctt ttc cag ttc ctg gtg ttc tac ttc ctc atc acc acc atg gct ttg 211
Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile Thr Thr Met Ala Leu
                                     25 30 35

tac gcc atc aag gaa ttt caa gcc tct gaa gta gaa gct ggc ttc gca 259
Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val Glu Ala Gly Phe Ala
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tcc agc tca att gtt atc ggc gca gtc ttt tcc agg ttt ttc tcc ggc 307
Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser Arg Phe Phe Ser Gly
                                     55 60 65

tat att att gac cgt ttt ggt cga cgc aag att gtg ctc atc tca gtc 355
Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile Val Leu Ile Ser Val
                                     70 75 80 85

cta gtc act acc att gcg tgt gcc ttg tac ctt ccc atc gaa tca ttg 403
Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu Pro Ile Glu Ser Leu
                                     90 95 100

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cca ttg cta tac gca aac agg ttc ctc cac ggt gtt gga tac gct ttt 451
 Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly Val Gly Tyr Ala Phe
 105 110 115

gct gcc acc gcg atc atg gca atg gtc cag gag ctc att cca gcg tca 499
 Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu Leu Ile Pro Ala Ser
 120 125 130

cga cgt tcc gaa ggt act ggt tac ctg gca ttg ggc act acc gtt tct 547
 Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu Gly Thr Thr Val Ser
 135 140 145

gca gca ctt gga cca gcc cta gca ctt ttt gtc cta gga aca ttt gat 595
 Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val Leu Gly Thr Phe Asp
 150 155 160 165

tac gac atg ctg ttt atc gtg gtc ttg gca acc tcg gtc atc tct ttg 643
 Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr Ser Val Ile Ser Leu
 170 175 180

atc gcc gtc gtg ttc atg tac ttt aag acc agc gac cct gag cct tct 691
 Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser Asp Pro Glu Pro Ser
 185 190 195

ggg gaa cca gcc aag ttc agc ttc aaa tct att atg aac cca aag atc 739
 Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile Met Asn Pro Lys Ile
 200 205 210

atc ccc atc ggc atc ttt atc ttg ctt att tgc ttt gct tac tct ggc 787
 Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys Phe Ala Tyr Ser Gly
 215 220 225

gtc att gcc tac atc aac gca ttt gct gaa gaa cgc gat ctg att acg 835
 Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu Arg Asp Leu Ile Thr
 230 235 240 245

ggt gct gga ttg ttc ttc att gcc tac gca gta tca atg ttt gtg atg 883
 Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val Ser Met Phe Val Met
 250 255 260

cgc agc ttc ctt ggc aaa ctg cag gac cgt cgc gga gac aac gtc gtt 931
 Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg Gly Asp Asn Val Val
 265 270 275

att tac ttt gga ttg ttc ttc ttc gtt att tcc ttg acg att ttg tcc 979
 Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser Leu Thr Ile Leu Ser
 280 285 290

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 295 300 305

ctg gga tac ggc act ttg atg cca gca gtg cag tcc atc gct gtt ggt 1075
 Leu Gly Tyr Gly Thr Leu Met Pro Ala Val Gln Ser Ile Ala Val Gly
 310 315 320 325

gta gta gac aaa acc gaa ttc ggt acg gcc ttc tcc act ttg ttc ctg 1123
 Val Val Asp Lys Thr Glu Phe Gly Thr Ala Phe Ser Thr Leu Phe Leu
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0960308-0

400> 182	Val	Ser	Val	Ala	Glu	Glu	Gly	Lys	Leu	Phe	Thr	Pro	Thr	Phe	Val	Met
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Gly	Trp	Phe	Ala	Asn	Leu	Phe	Gln	Phe	Leu	Val	Phe	Tyr	Phe	Leu	Ile	
			20						25					30		
Thr	Thr	Met	Ala	Leu	Tyr	Ala	Ile	Lys	Glu	Phe	Gln	Ala	Ser	Glu	Val	
			35					40					45			
Glu	Ala	Gly	Phe	Ala	Ser	Ser	Ser	Ile	Val	Ile	Gly	Ala	Val	Phe	Ser	
			50				55					60				
Arg	Phe	Phe	Ser	Gly	Tyr	Ile	Ile	Asp	Arg	Phe	Gly	Arg	Arg	Lys	Ile	
65					70					75					80	
Val	Leu	Ile	Ser	Val	Leu	Val	Thr	Thr	Ile	Ala	Cys	Ala	Leu	Tyr	Leu	
				85					90					95		
Pro	Ile	Glu	Ser	Leu	Pro	Leu	Leu	Tyr	Ala	Asn	Arg	Phe	Leu	His	Gly	
				100					105					110		
Val	Gly	Tyr	Ala	Phe	Ala	Ala	Thr	Ala	Ile	Met	Ala	Met	Val	Gln	Glu	
			115				120					125				
Leu	Ile	Pro	Ala	Ser	Arg	Arg	Ser	Glu	Gly	Thr	Gly	Tyr	Leu	Ala	Leu	
						135						140				
Gly	Thr	Thr	Val	Ser	Ala	Ala	Leu	Gly	Pro	Ala	Leu	Ala	Leu	Phe	Val	
145					150					155					160	
Leu	Gly	Thr	Phe	Asp	Tyr	Asp	Met	Leu	Phe	Ile	Val	Val	Leu	Ala	Thr	
				165					170					175		
Ser	Val	Ile	Ser	Leu	Ile	Ala	Val	Val	Phe	Met	Tyr	Phe	Lys	Thr	Ser	

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180
185
190
Asp Pro Glu Pro Ser Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile
195 200 205
Met Asn Pro Lys Ile Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys
210 215 220
Phe Ala Tyr Ser Gly Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu
225 230 235 240
Arg Asp Leu Ile Thr Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val
245 250 255
Ser Met Phe Val Met Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg
260 265 270
Gly Asp Asn Val Val Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser
275 280 285
Leu Thr Ile Leu Ser Phe Ala Thr Ser Asn Trp His Val Val Leu Ser
290 295 300
Gly Val Ile Ala Gly Leu Gly Tyr Gly Thr Leu Met Pro Ala Val Gln
305 310 315 320
Ser Ile Ala Val Gly Val Val Asp Lys Thr Glu Phe Gly Thr Ala Phe
325 330 335
Ser Thr Leu Phe Leu Phe Val Asp Leu Gly Phe Gly Phe Gly Pro Ile
340 345 350
Ile Leu Gly Ala Val Ser Ala Ala Ile Gly Phe Gly Pro Met Tyr Ala
355 360 365
Ala Leu Ala Gly Val Gly Val Ile Ala Gly Ile Phe Tyr Leu Phe Thr
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His Ala Arg Thr Asp Arg Ala Lys Asn Gly Phe Val Lys His Pro Glu
385 390 395 400
Pro Val Ala Leu Val Ser
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Val Ser Val Ala Glu
1 5

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gaa ggg aaa ctt ttt aca cca acg ttt gtc atg gga tgg ttt gcc aac 163
 Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met Gly Trp Phe Ala Asn
 10 15 20

ctt ttc cag ttc ctg gtg ttc tac ttc ctc atc acc acc atg gct ttg 211
 Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile Thr Thr Met Ala Leu
 25 30 35

tac gcc atc aag gaa ttt caa gcc tct gaa gta gaa gct ggc ttc gca 259
 Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val Glu Ala Gly Phe Ala
 40 45 50

tcc agc tca att gtt atc ggc gca gtc ttt tcc agg ttt ttc tcc ggc 307
 Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser Arg Phe Phe Ser Gly
 55 60 65

tat att att gac cgt ttt ggt cga cgc aag att gtg ctc atc tca gtc 355
 Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile Val Leu Ile Ser Val
 70 75 80 85

cta gtc act acc att gcg tgt gcc ttg tac ctt ccc atc gaa tca ttg 403
 Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu Pro Ile Glu Ser Leu
 90 95 100

cca ttg cta tac gca aac agg ttc ctc cac ggt gtt gga tac gct ttt 451
 Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly Val Gly Tyr Ala Phe
 105 110 115

gct gcc acc gcg atc atg gca atg gtc cag gag ctc att cca gcg tca 499
 Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu Leu Ile Pro Ala Ser
 120 125 130

cga cgt tcc gaa ggt act ggt tac ctg gca ttg ggc act acc gtt tct 547
 Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu Gly Thr Thr Val Ser
 135 140 145

gca gca ctt gga cca gcc cta gca ctt ttt gtc cta gga aca ttt gat 595
 Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val Leu Gly Thr Phe Asp
 150 155 160 165

tac gac atg ctg ttt atc gtg gtc ttg gca acc tcg gtc atc tct ttg 643
 Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr Ser Val Ile Ser Leu
 170 175 180

atc gcc gtc gtg ttc atg tac ttt aag acc agc gac cct gag cct tct 691
 Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser Asp Pro Glu Pro Ser
 185 190 195

ggg gaa cca gcc aag ttc agc ttc aaa tct att atg aac cca aag atc 739
 Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile Met Asn Pro Lys Ile
 200 205 210

atc ccc atc ggc atc ttt atc ttg ctt att tgc ttt gct tac tct ggc 787
 Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys Phe Ala Tyr Ser Gly
 215 220 225

gtc att gcc tac atc aac gca ttt gct gaa gaa cgc gat ctg att acg 835
 Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu Arg Asp Leu Ile Thr
 230 235 240 245

00602008-062300

ggt gct gga ttg ttc ttc att gcc tac gca gta tca atg ttt gtg atg 883
 Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val Ser Met Phe Val Met
 250 255 260

cgc agc ttc ctt ggc aaa ctg cag gac cgt cgc gga gac aac gtc gtt 931
 Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg Gly Asp Asn Val Val
 265 270 275

att tac ttt gga ttg ttc ttc ttc gtt att tcc ttg acg att ttg tcc 979
 Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser Leu Thr Ile Leu Ser
 280 285 290

ttt gcc act tcc aac tgg cac gtt gtg 1006
 Phe Ala Thr Ser Asn Trp His Val Val
 295 300

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 184
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Gly Trp Phe Ala Asn Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile
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Thr Thr Met Ala Leu Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val
 35 40 45

Glu Ala Gly Phe Ala Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser
 50 55 60

Arg Phe Phe Ser Gly Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile
 65 70 75 80

Val Leu Ile Ser Val Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu
 85 90 95

Pro Ile Glu Ser Leu Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly
 100 105 110

Val Gly Tyr Ala Phe Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu
 115 120 125

Leu Ile Pro Ala Ser Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu
 130 135 140

Gly Thr Thr Val Ser Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val
 145 150 155 160

Leu Gly Thr Phe Asp Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr
 165 170 175

Ser Val Ile Ser Leu Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser
 180 185 190

Asp Pro Glu Pro Ser Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile
 195 200 205

00603200-062300

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Met Asn Pro Lys Ile Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys
  210                      215                      220

Phe Ala Tyr Ser Gly Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu
  225                      230                      235                      240

Arg Asp Leu Ile Thr Gly Ala Gly Leu Phe Ile Ala Tyr Ala Val
                      245                      250                      255

Ser Met Phe Val Met Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg
                      260                      265                      270

Gly Asp Asn Val Val Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser
  275                      280                      285

Leu Thr Ile Leu Ser Phe Ala Thr Ser Asn Trp His Val Val
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<211> 568

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(568)

<223> RXA00858

<400> 185

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tcttaaattg  tctaaccaag  aaccggaggt  tctttttgtc  atg  gaa  gta  aac  tta      115
                      Met  Glu  Val  Asn  Leu
                      1                      5

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gcc aca tgg cta atc act atc gca gtg att gct ggc ttc ttc att ttc      163
Ala Thr Trp Leu Ile Thr Ile Ala Val Ile Ala Gly Phe Phe Ile Phe
                      10                      15                      20

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gat ttc tat tcc cac gtc cgc acc cca cac gag ccc act atc aaa gaa      211
Asp Phe Tyr Ser His Val Arg Thr Pro His Glu Pro Thr Ile Lys Glu
                      25                      30                      35

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```

tcc gca tgg tgg agc ctc ttc tac gta gcc ctc gcc tgt gtt ttc ggc      259
Ser Ala Trp Trp Ser Leu Phe Tyr Val Ala Leu Ala Cys Val Phe Gly
                      40                      45                      50

```

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gtg ttc ctc tgg ttt gct tgg ggc gag cca ggt aac cca cac cag cac      307
Val Phe Leu Trp Phe Ala Trp Gly Glu Pro Gly Asn Pro His Gln His
                      55                      60                      65

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ggc att gag ttc ttc acc ggt tac gtg aca gag aag gcg ttg agt gtt      355
Gly Ile Glu Phe Phe Thr Gly Tyr Val Thr Glu Lys Ala Leu Ser Val
                      70                      75                      80                      85

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gat aac ctc ttc atc ttc gcg ctg atc atg ggt tct ttc aag att cct      403
Asp Asn Leu Phe Ile Phe Ala Leu Ile Met Gly Ser Phe Lys Ile Pro
                      90                      95                      100

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[illegible]

<222> (101) .. (952)

<223> RXA02305

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caaacgatga cttcgatccc gaaaagtgga ggaacatgta atg cca gcc ttt gag 115
Met Pro Ala Phe Glu
1 5

gca atg cca gga atg ccg tat tgg atc gac ctg tcc acc tcg gac att 163
Ala Met Pro Gly Met Pro Tyr Trp Ile Asp Leu Ser Thr Ser Asp Ile
10 15 20

gca aaa tct gca cac ttc tac gaa aac gtt ctc ggc tgg gaa att gaa 211
Ala Lys Ser Ala His Phe Tyr Glu Asn Val Leu Gly Trp Glu Ile Glu
25 30 35

gaa gtc aac gat ggc tac cgc atg gct cgt ctg cag gga cta ccc gtg 259
Glu Val Asn Asp Gly Tyr Arg Met Ala Arg Leu Gln Gly Leu Pro Val
40 45 50

gca ggg ctg atc gat cag cgc ggt gaa tca agc atc ccg gat acc tgg 307
Ala Gly Leu Ile Asp Gln Arg Gly Glu Ser Ser Ile Pro Asp Thr Trp
55 60 65

att acc tac ttc ctc tcc tac gat ctg gat gcc act gca aag aag atc 355
Ile Thr Tyr Phe Leu Ser Tyr Asp Leu Asp Ala Thr Ala Lys Lys Ile
70 75 80 85

gca gaa ctg ggt gga cga att ctg gcc gag cca act gac gtg cac ttg 403
Ala Glu Leu Gly Gly Arg Ile Leu Ala Glu Pro Thr Asp Val His Leu
90 95 100

gga cgc atg atc cta gct gtt gat act gcc ggc gca ctg ttc ggc gtt 451
Gly Arg Met Ile Leu Ala Val Asp Thr Ala Gly Ala Leu Phe Gly Val
105 110 115

att gag cca ggc agc gag gaa tca ttc gtc gct gct ggt gaa cca ggc 49
Ile Glu Pro Gly Ser Glu Glu Ser Phe Val Ala Ala Gly Glu Pro Gly
120 125 130

aca tcc gtg tgg cat gaa ctc acc act gtc tcc aaa tat tcc gaa gct 54
Thr Ser Val Trp His Glu Leu Thr Thr Val Ser Lys Tyr Ser Glu Ala
135 140 145

atc gat ttc tac ggt gag ctg ttc act tgg aca acc tct gaa atg gct 59
Ile Asp Phe Tyr Gly Glu Leu Phe Thr Trp Thr Thr Ser Glu Met Ala
150 155 160 165

agt gct gaa gac gat agt ttc cgc tac acc acc gca ttg gct gac ggt 64
 Ser Ala Glu Asp Asp Ser Phe Arg Tyr Thr Thr Ala Leu Ala Asp Gly
 170 175 180

tcc gcc ttt gct gga att ttt gat gcc aaa ggc cac ttc cca cct cag 69
Ser Ala Phe Ala Gly Ile Phe Asp Ala Lys Gly His Phe Pro Pro Gln
185 190 195

ggt cca agc ttc tgg cag tcc tac ctt ggc gtg ctc aac gcc gat gat 73
Val Pro Ser Phe Trp Gln Ser Tyr Leu Gly Val Leu Asn Ala Asp Asp
200 205 210

096037436
in 063700

gct gca gcg aag gcc aag gaa ttt ggt ggc gat gtt att cgt aag coa 787
 Ala Ala Ala Lys Ala Lys Glu Phe Gly Gly Asp Val Ile Arg Lys Pro
 215 220 225

tgg gac tca gaa ttt ggc cgc atg gtt ctc atc tct gat tcc act ggt 835
 Trp Asp Ser Glu Phe Gly Arg Met Val Leu Ile Ser Asp Ser Thr Gly
 230 235 240 245

gcc aca att acc ttg tgt gaa gta gag gaa tac gtc gag gaa gca gca 883
 Ala Thr Ile Thr Leu Cys Glu Val Glu Glu Tyr Val Glu Glu Ala Ala
 250 255 260

gaa ggc gat gat ctc ttc gac atc gat ctc agt gct ttc gaa gag cag 931
 Glu Gly Asp Asp Leu Phe Asp Ile Asp Leu Ser Ala Phe Glu Glu Gln
 265 270 275

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 Phe Arg Lys Gln Glu Gly Gln
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<210> 188

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Met Pro Ala Phe Glu Ala Met Pro Gly Met Pro Tyr Trp Ile Asp Leu
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Ser Thr Ser Asp Ile Ala Lys Ser Ala His Phe Tyr Glu Asn Val Leu
 20 25 30

Gly Trp Glu Ile Glu Glu Val Asn Asp Gly Tyr Arg Met Ala Arg Leu
 35 40 45

Gln Gly Leu Pro Val Ala Gly Leu Ile Asp Gln Arg Gly Glu Ser Ser
 50 55 60

Ile Pro Asp Thr Trp Ile Thr Tyr Phe Leu Ser Tyr Asp Leu Asp Ala
 65 70 75 80

Thr Ala Lys Lys Ile Ala Glu Leu Gly Gly Arg Ile Leu Ala Glu Pro
 85 90 95

Thr Asp Val His Leu Gly Arg Met Ile Leu Ala Val Asp Thr Ala Gly
 100 105 110

Ala Leu Phe Gly Val Ile Glu Pro Gly Ser Glu Glu Ser Phe Val Ala
 115 120 125

Ala Gly Glu Pro Gly Thr Ser Val Trp His Glu Leu Thr Thr Val Ser
 130 135 140

Lys Tyr Ser Glu Ala Ile Asp Phe Tyr Gly Glu Leu Phe Thr Trp Thr
 145 150 155 160

Thr Ser Glu Met Ala Ser Ala Glu Asp Asp Ser Phe Arg Tyr Thr Thr
 165 170 175

00603208-0662300

	90	95	100	
gtc cga ccc gaa cta tgc gaa gta gac att gat atc tat ctt cac aac				451
Val Arg Pro Glu Leu Cys Glu Val Asp Ile Asp Ile Tyr Leu His Asn	105	110	115	
cct tcg gga cca gta tcc aga tgg gca aag aac tgc agt gtt gac gat				499
Pro Ser Gly Pro Val Ser Arg Trp Ala Lys Asn Cys Ser Val Asp Asp	120	125	130	
gaa cta atc atc acc ggc cct gac gta cgc gca gga gaa acc ggc tac				547
Glu Leu Ile Ile Thr Gly Pro Asp Val Arg Ala Gly Glu Thr Gly Tyr	135	140	145	
gga atc acc tat cat ccg act tct gcg atc gat cgc ctc tgt ctc atc				595
Gly Ile Thr Tyr His Pro Thr Ser Ala Ile Asp Arg Leu Cys Leu Ile	150	155	160	165
ggc gat tgt gca tca gct ccc gcg atc gca aat atc gtc aat caa tca				643
Gly Asp Cys Ala Ser Ala Pro Ala Ile Ala Asn Ile Val Asn Gln Ser	170		175	180
aaa gta cct act acg gtt ttc ctc cac gta gac agc cta gaa gat gat				691
Lys Val Pro Thr Thr Val Phe Leu His Val Asp Ser Leu Glu Asp Asp	185	190	195	
gta ttg atc gcc gat agc tcc acc aag ctc act ttc gaa gac atc gac				739
Val Leu Ile Ala Asp Ser Ser Thr Lys Leu Thr Phe Glu Asp Ile Asp	200	205	210	
gct tac aaa gca aag gtc ttc caa tgg gct tca gcc aat gca gca gat				787
Ala Tyr Lys Ala Lys Val Phe Gln Trp Ala Ser Ala Asn Ala Ala Asp	215	220	225	
cct tca gta cac ttc tgg atc gcc ggt gaa act agc atg gtg cgc ttc				835
Pro Ser Val His Phe Trp Ile Ala Gly Glu Thr Ser Met Val Arg Phe	230	235	240	245
att cgc aaa gaa cta atc aac agc tac cga gtt gat tcc tca cga atc				883
Ile Arg Lys Glu Leu Ile Asn Ser Tyr Arg Val Asp Ser Ser Arg Ile	250	255	260	
act ttc ctc ggc tac tgg aaa tac ggc cga cga acc gta gac				925
Thr Phe Leu Gly Tyr Trp Lys Tyr Gly Arg Arg Thr Val Asp	265	270	275	
tagctttcag attcagaccc cag				948
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Pro Val Gln Ile Ser Gln Lys Gln Arg Leu Ser Pro Gly Phe Met Arg	20	25	30	

00663200-062300

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Ile Thr Val Thr Gly Asp Lys Leu Arg Phe Phe Gly Gln Trp Gly Leu
   35                               40               45

Asp Gln Arg Ile Lys Leu Ile Ile Pro Ser Pro Ala Gly Asn Ile Pro
   50                               55               60

Asp Phe Gly Ile Leu Asp Glu Pro Thr Pro Pro Thr Thr Trp Leu
   65                               70               75               80

Pro Arg Ala Lys Ser Phe Pro Ala Asp Gln Arg Pro Ile Leu Arg Thr
   85                               90               95

Tyr Thr Pro Ser Ala Val Arg Pro Glu Leu Cys Glu Val Asp Ile Asp
  100                               105               110

Ile Tyr Leu His Asn Pro Ser Gly Pro Val Ser Arg Trp Ala Lys Asn
  115                               120               125

Cys Ser Val Asp Asp Glu Leu Ile Ile Thr Gly Pro Asp Val Arg Ala
  130                               135               140

Gly Glu Thr Gly Tyr Gly Ile Thr Tyr His Pro Thr Ser Ala Ile Asp
  145                               150               155               160

Arg Leu Cys Leu Ile Gly Asp Cys Ala Ser Ala Pro Ala Ile Ala Asn
  165                               170               175

Ile Val Asn Gln Ser Lys Val Pro Thr Thr Val Phe Leu His Val Asp
  180                               185               190

Ser Leu Glu Asp Asp Val Leu Ile Ala Asp Ser Ser Thr Lys Leu Thr
  195                               200               205

Phe Glu Asp Ile Asp Ala Tyr Lys Ala Lys Val Phe Gln Trp Ala Ser
  210                               215               220

Ala Asn Ala Ala Asp Pro Ser Val His Phe Trp Ile Ala Gly Glu Thr
  225                               230               235               240

Ser Met Val Arg Phe Ile Arg Lys Glu Leu Ile Asn Ser Tyr Arg Val
  245                               250               255

Asp Ser Ser Arg Ile Thr Phe Leu Gly Tyr Trp Lys Tyr Gly Arg Arg
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Thr Val Asp
  275

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<211> 468

<212> DNA

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<222> (101)..(445)

<223> RXA00843

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ttc cat aat ccg cgt tgt tcc aca tcc aga aat acc ctc gct tac ctc Phe His Asn Pro Arg Cys Ser Thr Ser Arg Asn Thr Leu Ala Tyr Leu	10 15 20	163
cgc gac aag gac att gag cct gaa att gtt cag tat ctc aaa gac acg Arg Asp Lys Asp Ile Glu Pro Glu Ile Val Gln Tyr Leu Lys Asp Thr	25 30 35	211
ccc acc gct tcc gag ctc aaa gaa cta ttc aat acg ctg gga att cca Pro Thr Ala Ser Glu Leu Lys Glu Leu Phe Asn Thr Thr Gly Ile Pro	40 45 50	259
gtc cac gac ggc atc aga acc cgc gaa gct gag tac aca gaa ctg ggc Val His Asp Gly Ile Arg Thr Arg Glu Ala Glu Tyr Thr Glu Leu Gly	55 60 65	307
ctg tca cca gaa aca cct gaa act gag ctt atc gac gcc atc gtt gcc Leu Ser Pro Glu Thr Pro Glu Thr Glu Leu Ile Asp Ala Ile Val Ala	70 75 80 85	355
cat ccc agg ctc ctt cag cgt ccg atc gtg gtg acg gcc aaa ggc gcg His Pro Arg Leu Leu Gln Arg Pro Ile Val Val Thr Ala Lys Gly Ala	90 95 100	403
cgc att gcg cgc ccc aaa atc gac gtc att gac agc atc ttg Arg Ile Ala Arg Pro Lys Ile Asp Val Ile Asp Ser Ile Leu	105 110 115	445
tgacaacatt ttgtagagca acc		468
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Thr Leu Ala Tyr Leu Arg Asp Lys Asp Ile Glu Pro Glu Ile Val Gln	20 25 30	
Tyr Leu Lys Asp Thr Pro Thr Ala Ser Glu Leu Lys Glu Leu Phe Asn	35 40 45	
Thr Leu Gly Ile Pro Val His Asp Gly Ile Arg Thr Arg Glu Ala Glu	50 55 60	
Tyr Thr Glu Leu Gly Leu Ser Pro Glu Thr Pro Glu Thr Glu Leu Ile	65 70 75 80	
Asp Ala Ile Val Ala His Pro Arg Leu Leu Gln Arg Pro Ile Val Val	85 90 95	
Thr Ala Lys Gly Ala Arg Ile Ala Arg Pro Lys Ile Asp Val Ile Asp		

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Ser Ile Leu			
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Met Asp Thr Lys Leu	5		
1			
ggc gct gaa ttg ggt act gaa ttt gat ctg att gtt gtt ggt ttc ggc	163		
Gly Ala Glu Leu Gly Thr Glu Phe Asp Leu Ile Val Val Gly Phe Gly	20		
10	15		
aaa gca ggc aag act atc gcg atg aaa cgc tcg gca gcg ggg gat aag	211		
Lys Ala Gly Lys Thr Ile Ala Met Lys Arg Ser Ala Ala Gly Asp Lys	35		
25	30		
gtc gca ctg atc gag cag agt cca cag atg tat ggc ggt acc tgc atc	259		
Val Ala Leu Ile Glu Gln Ser Pro Gln Met Tyr Gly Gly Thr Cys Ile	50		
40	45		
aat gta ggt tgc atc ccc acg aag aag ttg ttg ttt gag act gca acg	307		
Asn Val Gly Cys Ile Pro Thr Lys Lys Leu Leu Phe Glu Thr Ala Thr	65		
55	60		
ggc aag gat ttc ccg gat gcg gtt gtg gcg cgt gat cag ttg att ggc	355		
Gly Lys Asp Phe Pro Asp Ala Val Val Ala Arg Asp Gln Leu Ile Gly	85		
70	75	80	
aag ctg aat gcc aag aat ctt gcg atg gcc aca gac aag ggt gtc acc	403		
Lys Leu Asn Ala Lys Asn Leu Ala Met Ala Thr Asp Lys Gly Val Thr	100		
90	95		
cgt cat tgatggaaaa gctacgttta cag	432		
Arg His			
<210> 194			
<211> 103			
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1	5	10	15

Val Val Gly Phe Gly Lys Ala Gly Lys Thr Ile Ala Met Lys Arg Ser
 20 25 30

Ala Ala Gly Asp Lys Val Ala Leu Ile Glu Gln Ser Pro Gln Met Tyr
 35 40 45

Gly Gly Thr Cys Ile Asn Val Gly Cys Ile Pro Thr Lys Lys Leu Leu
 50 55 60

Phe Glu Thr Ala Thr Gly Lys Asp Phe Pro Asp Ala Val Val Ala Arg
 65 70 75 80

Asp Gln Leu Ile Gly Lys Leu Asn Ala Lys Asn Leu Ala Met Ala Thr
 85 90 95

Asp Lys Gly Val Thr Arg His
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 Val Leu Tyr Ala Pro
 1 5

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 Thr Ile Val Ile Asn Thr Gly Ser Thr Pro Val Ile Pro Asn Val Pro
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 Gly Thr Asp Asn Pro His Val Phe Asp Ser Thr Gly Ile Gln His Ile
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 Ser Pro Leu Pro Lys His Leu Ala Ile Ile Gly Gly Gly Pro Ile Gly
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 Ile Asp Arg Gly Glu Leu Pro Leu Lys Asn Phe Asp Arg Glu Val Ala
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Asp His Asp Leu Leu Ala Asp Ala Ala Leu Phe Ala Ser Ala Asp Ala
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Gly Gly Pro Ile Gly Leu Glu Phe Ala Thr Leu Phe Ser Gly Gln Gly
50 55 60

Ser Lys Val Thr Ile Ile Asp Arg Gly Glu Leu Pro Leu Lys Asn Phe
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Asp Arg Glu Val Ala Glu Leu Ala Lys Thr Asp Leu Glu Ala Arg Gly
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Ile Thr Phe Leu Asn Asn Ala Glu Leu Thr Gly Phe Ser Gly Asp Leu
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Val Leu Val Asp Ala

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cac ctc cgg acc aac atc gac ggc atc ttc gct gta ggt gat gtc aat 163
 His Leu Arg Thr Asn Ile Asp Gly Ile Phe Ala Val Gly Asp Val Asn
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 Gly Gly Pro Gln Phe Thr Tyr Val Ser Tyr Asp Asp His Arg Ile Val
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 Leu Asp Gln Leu Ala Gly Thr Gly Lys Lys Ser Ile Ala His Arg Leu
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 Asn Thr Glu Gly Glu Asn Val Val Val Lys Lys Ala Leu Ile Ala Asp
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 Met Pro Ile Val Pro Arg Pro Glu Ile Ile Asn Gln Pro His Gly Met
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 Met Arg His Gly Val Thr Ala Ser Glu Leu Gly Asp Gly Ile Tyr Thr
 135 140 145

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cga ggc cgg gga aag cct gaa gtc atg cgc tac cca gga att ccg ttc	Arg Gly Arg Gly Lys 10 Pro Glu Val Met 15 Tyr Pro Gly Ile Pro Phe 20	163
gcc atc cca gat cca gcg ccg cgt ggc ttc ctt ttc tta ggc gat etc	Ala Ile Pro Asp 25 Pro Ala Pro Arg Gly 30 Phe Leu Phe Leu Gly 35 Asp Leu	211
acc tct tac cca gcg atc tgc tcg att ctg gag acc ttg gac ggt gaa	Thr Ser Tyr Pro 40 Pro Ala Ile Cys Ser 45 Ile Leu Glu Thr 50 Leu Asp Gly Glu	259
atc cct gcg acc gcg tat ctt atc gcc cac gat cca ett gat tac acc	Ile Pro Ala Thr Ala Tyr 60 Leu Ile Ala His Asp 65 Pro Leu Asp Tyr Thr	307
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Met Gly Lys Gly Phe
1 5

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Thr Gly Ala Ile Leu Thr Val Met Gly Val Lys Ser His Ile Ala Thr
10 15 20

acc acg gga aaa acc gtg atc aat gac cgc atg gtg acc att cat ttt 211
Thr Thr Gly Lys Thr Val Ile Asn Asp Arg Met Val Thr Ile His Phe
25 30 35

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His Ser Glu Thr Leu Leu Asn Thr Glu Gly Glu Val Pro Gly Asp Trp
40 45 50

ctg cgt ctg tgg ttc ccg cac gag agc cga cct gga aag ctc tac caa 307
Leu Arg Leu Trp Phe Pro His Glu Ser Arg Pro Gly Lys Leu Tyr Gln
55 60 65

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 Arg Ala Tyr Thr Leu Thr Asn Val Asp Ala Asp Ala Gly Thr Phe Asp
 70 75 80 85

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Leu Ala Phe Val Leu His Glu Pro Leu Gly Pro Ala Ser Ala Trp Ala
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Thr Arg Cys Glu Ala Gly Glu Ser Leu Glu Val Met Arg Tyr Pro Gly
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185 190 195

acc gat ttt tat acc tgg atc ggc gcg gaa tcc tcc gaa acc cgt 736

Case	Age	Sex	Duration	Location	Findings	Comments
1	10	M	10 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
2	12	F	15 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
3	15	M	20 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
4	18	F	25 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
5	20	M	30 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
6	22	F	35 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
7	25	M	40 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
8	28	F	45 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
9	30	M	50 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
10	32	F	55 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
11	35	M	60 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
12	38	F	65 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
13	40	M	70 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
14	42	F	75 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
15	45	M	80 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
16	48	F	85 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
17	50	M	90 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
18	52	F	95 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
19	55	M	100 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
20	58	F	105 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
21	60	M	110 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
22	62	F	115 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
23	65	M	120 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
24	68	F	125 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
25	70	M	130 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
26	72	F	135 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
27	75	M	140 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
28	78	F	145 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
29	80	M	150 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
30	82	F	155 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
31	85	M	160 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
32	88	F	165 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
33	90	M	170 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
34	92	F	175 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
35	95	M	180 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
36	98	F	185 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
37	100	M	190 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
38	102	F	195 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
39	105	M	200 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
40	108	F	205 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
41	110	M	210 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
42	112	F	215 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
43	115	M	220 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
44	118	F	225 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
45	120	M	230 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
46	122	F	235 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
47	125	M	240 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
48	128	F	245 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
49	130	M	250 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
50	132	F	255 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
51	135	M	260 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
52	138	F	265 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
53	140	M	270 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
54	142	F	275 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
55	145	M	280 days	Left eye	Corneal opacity, anterior chamber cells	Acute inflammation
56	148	F	285 days	Right eye	Corneal opacity, anterior chamber cells	Acute inflammation
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 <213> *Corynebacterium glutamicum*
 <400> 206
 Met Ser Gln Ala Ile Asp Ser Lys Val Glu Ala His Glu Gly His Glu
 1 5 10 15
 Gly His Glu Gly Ile Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val
 20 25 30
 Phe Ala Met Leu Ala Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys
 35 40 45

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Thr Gln Ala Leu Leu Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro
 50 55 60
 Thr Glu Ser Ala Leu Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu
 65 70 75 80
 Cys Ile Val Pro Ala Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg
 85 90 95
 Val Leu Thr Ile Ser Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu
 100 105 110
 Pro Leu Val Pro Asn Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln
 115 120 125
 Gly Ala Leu Leu Ala Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser
 130 135 140
 Glu Glu Ile His Pro Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile
 145 150 155 160
 Ala Gly Asn Thr Val Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly
 165 170 175
 Leu Leu Glu Val Thr His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile
 180 185 190
 Ala Ala Leu Ile Phe Gly Val Ile Met Val Val Leu Leu Pro Lys Gln
 195 200 205
 Arg Lys Phe Gln Pro Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala
 210 215 220
 Met Ala Ala His Trp Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr
 225 230 235 240
 Ala Phe Leu Gly Met Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly
 245 250 255
 Phe Arg Met Ile Asp Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala
 260 265 270
 Val Phe Ile Met Tyr Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly
 275 280 285
 Ala Leu Arg Glu Lys Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser
 290 295 300
 Leu Thr Met Ile Ala Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp
 305 310 315 320
 Val Thr Leu Val Ala Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu
 325 330 335
 His Ser Ser Ala Ser Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg
 340 345 350
 Ala Glu Ala Ser Ser Met Tyr Leu Phe Cys Tyr Tyr Val Gly Ser Ser
 355 360 365

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135	140	145	
aag gat att ggg cat gcg atg gga att tac atc gcg gga aat act gtc Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile Ala Gly Asn Thr Val 150 155 160 165			595
ggc ggg ctc act gga cgt atg att ccg gcg gga cta ctt gaa gta act Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly Leu Leu Glu Val Thr 170 175 180			643
cat tgg caa aac gca ctg ctg gga agt tct atc gct gcg ctg atc ttc His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile Ala Ala Leu Ile Phe 185 190 195			691
ggc gta atc atg gtg gtg ttg ctt ccc aag cag cgg aaa ttc cag ccg Gly Val Ile Met Val Val Leu Leu Pro Lys Gln Arg Lys Phe Gln Pro 200 205 210			739
aag aat atc aat ctg cgc cat gag att tcg gcg atg gct gct cat tgg Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala Met Ala Ala His Trp 215 220 225			787
cgg aat cct cgt ttg gcg ttg ctt ttt ggt act gcg ttt ttg ggc atg Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr Ala Phe Leu Gly Met 230 235 240 245			835
ggt act ttt gtg tcg ctg tac aac tat ttg ggt ttc cgc atg att gat Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly Phe Arg Met Ile Asp 250 255 260			883
cag ttt ggg ctg agt gaa gtg ctg gtt ggt gcg gtg ttc atc atg tat Gln Phe Gly Leu Ser Glu Val Leu Leu Gly Ala Val Phe Ile Met Tyr 265 270 275			931
ctg gcc ggg acc tgg agt tcc acc cag gcg ggt gcg ttg agg gag aag Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly Ala Leu Arg Glu Lys 280 285 290			979
atc ggc aat ggg tca acg gtt att ttc ttg agt ctg acg atg atc gcg Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser Leu Thr Met Ile Ala 295 300 305			1027
tcg atg gca ctg atg ggg att aat aat ttg tgg gtc acg ttg gtt gcc Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp Val Thr Leu Val Ala 310 315 320 325			1075
ctg ttt gtg ttt acc gcg gca ttt ttc gca ctg cat tcc agt gct tcg Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu His Ser Ser Ala Ser 330 335 340			1123
gga tgg atc gga atc atc gca acg aag gat cgc gcg gaa gcc tcc agc Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg Ala Glu Ala Ser Ser 345 350 355			1171
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<210> 208

<211> 364

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 208

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Met Ser Gln Ala Ile Asp Ser Lys Val Glu Ala His Glu Gly His Glu
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Gly His Glu Gly Ile Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val
      20           25           30

Phe Ala Met Leu Ala Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys
      35           40           45

Thr Gln Ala Leu Leu Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro
      50           55           60

Thr Glu Ser Ala Leu Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu
      65           70           75           80

Cys Ile Val Pro Ala Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg
      85           90           95

Val Leu Thr Ile Ser Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu
      100          105          110

Pro Leu Val Pro Asn Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln
      115          120          125

Gly Ala Leu Leu Ala Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser
      130          135          140

Glu Glu Ile His Pro Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile
      145          150          155          160

Ala Gly Asn Thr Val Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly
      165          170          175

Leu Leu Glu Val Thr His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile
      180          185          190

Ala Ala Leu Ile Phe Gly Val Ile Met Val Val Leu Leu Pro Lys Gln
      195          200          205

Arg Lys Phe Gln Pro Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala
      210          215          220

Met Ala Ala His Trp Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr
      225          230          235          240

Ala Phe Leu Gly Met Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly
      245          250          255

Phe Arg Met Ile Asp Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala
      260          265          270

Val Phe Ile Met Tyr Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly
      275          280          285

Ala Leu Arg Glu Lys Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser
      290          295          300

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00660208-062300

Leu Thr Met Ile Ala Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp
305 310 315 320

Val Thr Leu Val Ala Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu
325 330 335

His Ser Ser Ala Ser Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg
340 345 350

Ala Glu Ala Ser Ser Met Tyr Leu Phe Cys Glu Tyr
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<210> 209

<211> 1572

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1549)

<223> RXN00034

<400> 209

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ttttgcaagt ttctatagat tgatagaaaa gggagtttag atg tct tac aca tct 115
Met Ser Tyr Thr Ser
1 5

ttt aaa ggc gat gat aaa gcc ctc atc ggc ata gtt tta tca gtt ctc 163
Phe Lys Gly Asp Asp Lys Ala Leu Ile Gly Ile Val Leu Ser Val Leu
10 15 20

aca ttt tgg ctt ttt gct cag tca acc cta aat atc ggc cca gat atg 211
Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn Ile Gly Pro Asp Met
25 30 35

gca act gat tta ggg atg agc gat gcc acc atg aac ata gct gtc gtg 259
Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met Asn Ile Ala Val Val
40 45 50

gcc gcc gcg tta ttc tgt gga aca ttt atc gtc gca gcc gcc gcc atc 307
Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val Ala Ala Gly Gly Ile
55 60 65

gca gat gtc ttt ggc cga gta cga atc atg atg att gcc aac atc ott 355
Ala Asp Val Phe Gly Arg Val Arg Ile Met Met Ile Gly Asn Ile Leu
70 75 80 85

aac atc ctg gga tct ctc ctc atc gcc acg gca acg act tct tta gcc 403
Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala Thr Ser Leu Ala
90 95 100

acc caa atg gtg atc acc gcc cga gtt ctc caa gga ctg gca gca gcg 451
Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln Gly Leu Ala Ala Ala
105 110 115

gcc atc atg tct gca tcc cta gca tta gtt aag aca tat tgg tta ggt 499
Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys Thr Tyr Trp Leu Gly
120 125 130

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act gac cgc caa cga gca gtc tcc att tgg tcc att ggt tca tgg ggt 547
 Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser Ile Gly Ser Trp Gly
 135 140 145

ggc acc gga ttc tgc gcg ctt ttc gcg ggt ctt gtt gta gca agc ccc 595
 Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu Val Val Ala Ser Pro
 150 155 160 165

ttt ggt tgg aga gga atc ttc gcc ctc tgc gcg atc gtc tcc atc gtt 643
 Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala Ile Val Ser Ile Val
 170 175 180

gct att gcc ctt acc cgc cac atc ccg gaa tcc cgt ccg gct caa tcc 691
 Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser Arg Pro Ala Gln Ser
 185 190 195

att ggc atg cat ttg gat tgg agt ggc atc atc gtt ctt gcc ctc agt 739
 Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile Val Leu Ala Leu Ser
 200 205 210

gtt cta tct ctt gaa ttg ttt att acc caa ggt gaa tca ctt ggc tgg 787
 Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly Glu Ser Leu Gly Trp
 215 220 225

acg cac tgg atg acc tgg act ctc ctt gcc gtt tct ttg aca ttt ctt 835
 Thr His Trp Met Thr Trp Thr Leu Leu Ala Val Ser Leu Thr Phe Leu
 230 235 240 245

gca gtt ttc gtc ttc att gaa cgc atc gcc agc tgg cca gtt ctc gac 883
 Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser Trp Pro Val Leu Asp
 250 255 260

ttc aac ctt ttc aaa gac cac gcc ttc agc ggt gcg acc atc acc aac 931
 Phe Asn Leu Phe Phe Lys Asp His Ala Phe Ser Gly Ala Thr Ile Thr Asn
 265 270 275

ttc att atg agc gct act ggc gga gta gtt gcc gtt gtc atg tgg gtt 979
 Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala Val Val Met Trp Val
 280 285 290

cag caa atg gga tgg ggt gtc tcc cca aca atc tgc gga ctc acc agc 1027
 Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile Ser Gly Leu Thr Ser
 295 300 305

atc ggc ttc gca gcc ttt gtc atc ctt ttc att cga gtt gga gaa aag 1075
 Ile Gly Phe Ala Ala Phe Val Ile Leu Phe Ile Arg Val Gly Glu Lys
 310 315 320 325

gcc atg cag aaa gtt ggc gcc cga gca gtg atc atc acc gct ggc atc 1123
 Ala Met Gln Lys Val Gly Ala Arg Ala Val Ile Ile Thr Ala Gly Ile
 330 335 340

ttg gta gcg acc gcg acc gcc ctc cta atg atc acc gcg gtc agc gag 1171
 Leu Val Ala Thr Ala Thr Ala Leu Met Ile Thr Ala Val Ser Glu
 345 350 355

tca acg tac atc gtc atc tcc ctc gcc ggc ttc tcc ctt tat ggc ett 1219
 Ser Thr Tyr Ile Val Ile Ser Leu Ala Gly Phe Ser Leu Tyr Gly Leu
 360 365 370

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ggc ctc gga ctc ttc gcc acc cca gtc acc gat act gcg ctt gga aca 1267
 Gly Leu Gly Leu Phe Ala Thr Pro Val Thr Asp Thr Ala Leu Gly Thr
 375 380 385

ctt ccc aaa gac cgt acc ggc gct ggt gca ggt gta ttc aag atg tcc 1315
 Leu Pro Lys Asp Arg Thr Gly Ala Gly Ala Gly Val Phe Lys Met Ser
 390 395 400 405

tct tcc ctc ggc gca gca ctc ggc atc gca atc tcc act tca gtg ttc 1363
 Ser Ser Leu Gly Ala Ala Leu Gly Ile Ala Ile Ser Thr Ser Val Phe
 410 415 420

ctc gca ctt cgc gac ggc acc tcc atc aac tcc gac gtc gca ctc gcc 1411
 Leu Ala Leu Arg Asp Gly Thr Ser Ile Asn Ser Asp Val Ala Leu Ala
 425 430 435

gga aca gtt tca ctt ggc atc aac gtt gta ttc gca gca aca gcc acc 1459
 Gly Thr Val Ser Leu Gly Ile Asn Val Val Phe Ala Ala Thr Ala Thr
 440 445 450

atc acc gca gca gtc ctt att cca aaa gcc gct ggc aaa gtc tca caa 1507
 Ile Thr Ala Ala Val Leu Ile Pro Lys Ala Ala Gly Lys Val Ser Gln
 455 460 465

acc agc atc acc ctt cct gag cca gct atc gct gta aaa atc 1549
 Thr Ser Ile Thr Leu Pro Glu Pro Ala Ile Ala Val Lys Ile
 470 475 480

taaaacttca ccaggacaga taa 1572

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 <212> FRT
 <213> Corynebacterium glutamicum

<400> 210
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Val Leu Ser Val Leu Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn
 20 25 30

Ile Gly Pro Asp Met Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met
 35 40 45

Asn Ile Ala Val Val Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val
 50 55 60

Ala Ala Gly Gly Ile Ala Asp Val Phe Gly Arg Val Arg Ile Met Met
 65 70 75 80

Ile Gly Asn Ile Leu Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala
 85 90 95

Thr Thr Ser Leu Ala Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln
 100 105 110

Gly Leu Ala Ala Ala Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys
 115 120 125

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Thr	Tyr	Trp	Leu	Gly	Thr	Asp	Arg	Gln	Arg	Ala	Val	Ser	Ile	Trp	Ser
130						135					140				
Ile	Gly	Ser	Trp	Gly	Gly	Thr	Gly	Phe	Cys	Ala	Leu	Phe	Ala	Gly	Leu
145				150						155					160
Val	Val	Ala	Ser	Pro	Phe	Gly	Trp	Arg	Gly	Ile	Phe	Ala	Leu	Cys	Ala
				165					170					175	
Ile	Val	Ser	Ile	Val	Ala	Ile	Ala	Leu	Thr	Arg	His	Ile	Pro	Glu	Ser
			180						185				190		
Arg	Pro	Ala	Gln	Ser	Ile	Gly	Met	His	Leu	Asp	Trp	Ser	Gly	Ile	Ile
		195					200					205			
Val	Leu	Ala	Leu	Ser	Val	Leu	Ser	Leu	Glu	Leu	Phe	Ile	Thr	Gln	Gly
	210					215					220				
Glu	Ser	Leu	Gly	Trp	Thr	His	Trp	Met	Thr	Trp	Thr	Leu	Leu	Ala	Val
225					230					235				240	
Ser	Leu	Thr	Phe	Leu	Ala	Val	Phe	Val	Phe	Ile	Glu	Arg	Ile	Ala	Ser
			245					250						255	
Trp	Pro	Val	Leu	Asp	Phe	Asn	Leu	Phe	Lys	Asp	His	Ala	Phe	Ser	Gly
		260						265					270		
Ala	Thr	Ile	Thr	Asn	Phe	Ile	Met	Ser	Ala	Thr	Gly	Gly	Val	Val	Ala
		275					280					285			
Val	Val	Met	Trp	Val	Gln	Gln	Met	Gly	Trp	Gly	Val	Ser	Pro	Thr	Ile
	290					295					300				
Ser	Gly	Leu	Thr	Ser	Ile	Gly	Phe	Ala	Ala	Phe	Val	Ile	Leu	Phe	Ile
305					310					315				320	
Arg	Val	Gly	Glu	Lys	Ala	Met	Gln	Lys	Val	Gly	Ala	Arg	Ala	Val	Ile
				325					330					335	
Ile	Thr	Ala	Gly	Ile	Leu	Val	Ala	Thr	Ala	Thr	Ala	Leu	Leu	Met	Ile
		340						345					350		
Thr	Ala	Val	Ser	Glu	Ser	Thr	Tyr	Ile	Val	Ile	Ser	Leu	Ala	Gly	Phe
	355						360					365			
Ser	Leu	Tyr	Gly	Leu	Gly	Leu	Gly	Leu	Phe	Ala	Thr	Pro	Val	Thr	Asp
	370					375					380				
Thr	Ala	Leu	Gly	Thr	Leu	Pro	Lys	Asp	Arg	Thr	Gly	Ala	Gly	Ala	Gly
385					390					395					400
Val	Phe	Lys	Met	Ser	Ser	Ser	Leu	Gly	Ala	Ala	Leu	Gly	Ile	Ala	Ile
			405						410					415	
Ser	Thr	Ser	Val	Phe	Leu	Ala	Leu	Arg	Asp	Gly	Thr	Ser	Ile	Asn	Ser
		420						425					430		
Asp	Val	Ala	Leu	Ala	Gly	Thr	Val	Ser	Leu	Gly	Ile	Asn	Val	Val	Phe
	435						440						445		
Ala	Ala	Thr	Ala	Thr	Ile	Thr	Ala	Ala	Val	Leu	Ile	Pro	Lys	Ala	Ala

A

450					455					460					
Gly	Lys	Val	Ser	Gln	Thr	Ser	Ile	Thr	Leu	Pro	Glu	Pro	Ala	Ile	Ala
465					470					475					480

Val Lys Ile

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<211> 1045
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1045)
<223> FRXA02273
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				Met Ser Tyr	Thr Ser		
ttt aaa ggc gat	gat aaa gcc ctc atc ggc ata gtt tta tca gtt ctc						163
Phe Lys Gly Asp	Asp Lys Ala Leu Ile Gly Ile Val Leu Ser Val Leu						
	10	15	20				
aca ttt tgg ctt ttt gct cag tca acc cta aat atc ggc cca gat atg							211
Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn Ile Gly Pro Asp Met							
	25	30	35				
gca act gat tta ggg atg agc gat ggc acc atg aac ata gct gtc gtg							259
Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met Asn Ile Ala Val Val							
	40	45	50				
gcc gcc gcg tta ttc tgt gga aca ttt atc gtc gca gcc ggc ggc atc							307
Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val Ala Ala Gly Gly Ile							
	55	60	65				
gca gat gtc ttt ggc cga gta cga atc atg atg att ggc aac atc ctt							355
Ala Asp Val Phe Gly Arg Val Arg Ile Met Met Ile Gly Asn Ile Leu							
	70	75	80				
aac atc ctg gga tct ctc ctc atc gcc acg gca acg act tct tta gcc							403
Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala Thr Thr Ser Leu Ala							
	90	95	100				
acc caa atg gtg atc acc ggc cga gtt ctc caa gga ctg gca gca gcg							451
Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln Gly Leu Ala Ala Ala							
	105	110	115				
gcc atc atg tct gca tcc cta gca tta gtt aag aca tat tgg tta ggt							499
Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys Thr Tyr Trp Leu Gly							
	120	125	130				
act gac cgc caa cga gca gtc tcc att tgg tcc att ggt tca tgg ggt							547
Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser Ile Gly Ser Trp Gly							
	135	140	145				

0963030E
in
DFAEDC

ggc acc gga ttc tgc gcg ctt ttc gcg ggt ctt gtt gta gca agc ccc 595
 Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu Val Val Ala Ser Pro
 150 155 160 165

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 Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala Ile Val Ser Ile Val
 170 175 180

 gct att gcc ctt acc cgc cac atc ccg gaa tcc cgt ccg gct caa tcc 691
 Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser Arg Pro Ala Gln Ser
 185 190 195

 att ggc atg cat ttg gat tgg agt ggc atc atc gtt ctt gcc ctc agt 739
 Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile Val Leu Ala Leu Ser
 200 205 210

 gtt cta tct ctt gaa ttg ttt att acc caa ggt gaa tca ctt ggc tgg 787
 Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly Glu Ser Leu Gly Trp
 215 220 225

 acg cac tgg atg acc tgg act ctc ctt gcc gtt tct ttg aca ttt ctt 835
 Thr His Trp Met Thr Trp Thr Leu Leu Ala Val Ser Leu Thr Phe Leu
 230 235 240 245

 gca gtt ttc gtc ttc att gaa cgc atc gcc agc tgg cca gtt ctc gac 883
 Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser Trp Pro Val Leu Asp
 250 255 260

 ttc aac ctt ttc aaa gac cac gcc ttc agc ggt gcg acc atc acc aac 931
 Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly Ala Thr Ile Thr Asn
 265 270 275

 ttc att atg agc gct act ggc gga gta gtt gcc gtt gtc atg tgg gtt 979
 Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala Val Met Trp Val
 280 285 290

 cag caa atg gga tgg ggt gtc tcc cca aca atc tgc gga ctc acc agc 1027
 Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile Ser Gly Leu Thr Ser
 295 300 305

 atc ggc ttc gca gcc ttt 1045
 Ile Gly Phe Ala Ala Phe
 310 315

<210> 212
 <211> 315
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 <213> Corynebacterium glutamicum

<400> 212
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 20 25 30

 Ile Gly Pro Asp Met Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met
 35 40 45

006603208-066200

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Asn Ile Ala Val Val Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val
  50                      55                      60

Ala Ala Gly Gly Ile Ala Asp Val Phe Gly Arg Val Arg Ile Met Met
  65                      70                      75                      80

Ile Gly Asn Ile Leu Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala
                      85                      90                      95

Thr Thr Ser Leu Ala Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln
 100                      105                      110

Gly Leu Ala Ala Ala Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys
 115                      120                      125

Thr Tyr Trp Leu Gly Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser
 130                      135                      140

Ile Gly Ser Trp Gly Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu
 145                      150                      155                      160

Val Val Ala Ser Pro Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala
                      165                      170                      175

Ile Val Ser Ile Val Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser
                      180                      185                      190

Arg Pro Ala Gln Ser Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile
 195                      200                      205

Val Leu Ala Leu Ser Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly
 210                      215                      220

Glu Ser Leu Gly Trp Thr His Trp Met Thr Trp Thr Leu Leu Ala Val
 225                      230                      235                      240

Ser Leu Thr Phe Leu Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser
                      245                      250                      255

Trp Pro Val Leu Asp Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly
 260                      265                      270

Ala Thr Ile Thr Asn Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala
 275                      280                      285

Val Val Met Trp Val Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile
 290                      295                      300

Ser Gly Leu Thr Ser Ile Gly Phe Ala Ala Phe
 305                      310                      315

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<211> 826
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> RXN03075

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							Val	Ala	Lys	Phe	Leu	5					
tat aag tta ggc tcc acg gcc tat caa aag aaa tgg cgg ttt ctt gcg	163																
Tyr Lys Leu Gly Ser 10 Thr Ala Tyr Gln Lys 15 Trp Pro Phe Leu Ala 20																	
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Val Trp Leu Val Ile 25 Leu Ile Gly Ile 30 Thr Thr Leu Ala Gly Leu Tyr 35																	
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Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val 40 50																	
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Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala 55 60 65																	
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Thr Ser Ala Pro Thr Gly Ser Val Val Ile 70 75 80 85																	
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Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp 90 95 100																	
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Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val 185 190 195																	
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Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr
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Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro
 35 40 45

Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro
 50 55 60

Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
 65 70 75 80

Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
 85 90 95

Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
 100 105 110

Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
 115 120 125

Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
 130 135 140

Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
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Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala
 165 170 175

Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
 180 185 190

Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr
 195 200 205

Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
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 225 230 235 240

Ile Ser

00603208-062300

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				Val	Ala	Lys	Phe	Leu	5										
tat aag	tta ggc	tcc acg	gcc tat	caa aag	aaa	tgg	ccg	ttt	ctt	gcg	163								
Tyr Lys	Leu Gly	Ser Thr	Ala Tyr	Gln Lys	Lys Trp	Pro	Phe	Leu	20	Ala									
				10	15														
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Val Trp	Leu Val	Ile Leu	Ile Ile	Gly Ile	Thr Thr	Leu	Ala	Gly	Leu	Tyr									
				25	30							35							
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Ala Lys	Pro Thr	Ser Ser	Ser Phe	Ser Ile	Pro Gly	Leu Asp	Ser Val												
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Thr Thr	Met Glu	Lys Met	Gln Glu	Arg Phe	Pro Gly	Ser Asp	Asp Ala												
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Thr Ser	Ala Pro	Thr Gly	Ser Val	Val Val	Ile Gln	Ala Pro	Glu Gly	Lys											
				70	75	80	85												
acc ctc	act gat	cct gag	gtt ggg	gct gaa	gta aac	cag atg	ctt gat	403											
Thr Leu	Thr Asp	Pro Glu	Val Gly	Ala Ala	Glu Val	Asn Gln	Met Leu	100											
				90	95														
gag gtt	cgg gcg	act ggt	gtg ctg	aag gat	gct gat	tcc gtt	gtg gat	451											
Glu Val	Arg Ala	Thr Gly	Val Leu	Lys Asp	Ala Asp	Ser Val	Val Asp												
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cct gtg	ttg gct	gcg cag	ggt gtg	gct gct	cag atg	acc cca	gcc ctg	499											
Pro Val	Leu Ala	Ala Gln	Gly Val	Ala Ala	Gln Met	Thr Pro	Ala Leu												
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Glu Ala	Gln Gly	Val Pro	Ala Glu	Lys Ile	Ala Ala	Asp Ile	Glu Ser												
				135	140	145													
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Ile Ser	Pro Leu	Ser Ala	Asp Glu	Thr Thr	Gly Ile	Ile Ser	Met Thr												
				150	155	160	165												
ttt gat	gca gat	tct gcc	atg gat	ata tcc	gca gag	gat cgt	gag aag	643											
Phe Asp	Ala Asp	Ser Ala	Met Asp	Ile Ser	Ala Glu	Asp Arg	Glu Lys												

0960328-05200


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tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc 739
Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr Ser Leu Asp Met Thr
200              205              210

tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc 787
Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr
215              220              225

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Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro
35      40      45

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Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
65      70      75      80

Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
85      90      95

Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
100     105     110

Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
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Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
130     135     140

Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
145     150     155     160

Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala
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Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
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00602208.066200

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Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
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Ile Ser

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 Met Ser Thr Ser Ile
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aca aca gag aac aag aag aaa tct ggt cct cct cgc ttg atg aga atc 163
 Thr Thr Glu Asn Lys Lys Ser Gly Pro Pro Arg Leu Met Arg Ile
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ttt ctg ccc gcc ttg cta att tta gtt tgg ctt gta gga gct gga gtc 211
 Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu Val Gly Ala Gly Val
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ggc ggt cct tat ttt ggc aag gtt agt gag gtc tcc tcc aac agc cag 259
 Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val Ser Ser Asn Ser Gln
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acc aca tat ctg cca gaa tct gcc gat gcc act caa gta cag gaa cag 307
 Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr Gln Val Gln Glu Gln
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gtc agc gat gaa ccc tta aca cag caa gac atc aca caa ctc aat gaa 403
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 90 95 100

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 Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val Ser Asp Glu Val Ser
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cct gct att cca tcc gag gac gcc aga gct gtc caa gtg ttt gtc ccc 499
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 Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala Phe Ala Gly Ile Asp
 170 175 180

ggg cta ctc cta gca gtc gcc ttg gct gcc gtc ctt gtc att ctt gtc 691
 Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val Leu Val Ile Leu Val
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atc gtc tat cgc tcc ttc att ctg ccc atc gcc gtg ctt gcc acc agt 739
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 200 205 210

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 230 235 240 245

ctg gtc att ggc gcc gcc acc gac tac tca ttg cta tac gtt gct cgt 883
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 Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile Ile Phe Ala Met Leu
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 Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe Val Phe Gly Arg Val
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 Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro Glu Lys Ala Arg Ala
 345 350 355

aaa aac gac atc ccc gcc agc ggg atc tgg tca aaa gtg gct gat tta 1219
 Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser Lys Val Ala Asp Leu
 360 365 370

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375 380 385	
ctc ttg ggt gcg gct ttc gtt ccc aca cta aaa gcg gac ggt gtg tcc	1315
Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys Ala Asp Gly Val Ser	
390 395 400 405	
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Gln Ser Asp Leu Val Leu Gly Ser Ser Ala Ala Arg Asp Gly Gln Gln	
410 415 420	
gct tta ggc gaa cac ttc ccc ggt gga tcc ggc agt cct gct tat att	1411
Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly Ser Pro Ala Tyr Ile	
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Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala Asp Val Val Leu Asn	
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Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val Pro Leu Gly Ser Gly	
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Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val Ile Leu Val Ile Leu	
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Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val Ala Ala Leu Leu Phe	
585 590 595	
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Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro Ala Val Pro Leu Tyr	
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 Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His Gly Thr Arg Leu Gly
 630 635 640 645
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 Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser Asn Gln Lys Tyr Gln
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 100 105 110
 Ser Asp Glu Val Ser Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val
 115 120 125

002290-80220960

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 Glu Lys Leu Ser Glu Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser
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 Phe Ala Gly Ile Asp Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val
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 Val Leu Ala Thr Ser Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val
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 Trp Trp Leu Ala Lys Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln
 225 230 235 240
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 Gly Ile Ala Thr Gly Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu
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 Asp Leu Lys Ser Asn Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile
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 325 330 335
 Val Phe Gly Arg Val Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro
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 Glu Lys Ala Arg Ala Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser
 355 360 365
 Lys Val Ala Asp Leu Val Glu Gln His Pro Arg Ala Ile Trp Val Ser
 370 375 380
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 Ala Asp Gly Val Ser Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala
 405 410 415
 Arg Asp Gly Gln Gln Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly
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 Ser Pro Ala Tyr Ile Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala
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006390-8023060

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Ala Asp Ser Pro Ser Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val
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Pro Leu Gly Ser Gly Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln
  485                               490                               495

Val Leu Leu Gln Ala Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala
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Gln Lys Ala Ile Arg Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile
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Ser Ala Val Val Gly Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp
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Ala Ser Ile His Asp Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val
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Leu Leu Val Val Thr Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val
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Ala Ala Leu Leu Phe Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro
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Ala Val Pro Leu Tyr Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp
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Tyr Asn Ile Phe Leu Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His
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Gly Thr Arg Leu Gly Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val
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Val Ile Pro Ile Leu Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe
  675                               680                               685

Gly Val Leu Ile Asp Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala
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Leu Phe Tyr Asp Ile Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser
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gat acc gcg cag atc ctg tta ccc cag aat ttg atg cga tcg atg agc	816
Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser	
260 265 270	
gca cct ctg aga ctc tcg caa ctc ttc gtg cag atg ctg aga cct tcg	864
Ala Pro Leu Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser	
275 280 285	
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Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe	
290 295 300	
acg atg aca tct ctg ctc gcc tcg gcg acg tcc tgg ttc ctt acg ttc	960
Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe	
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<213> <i>Corynebacterium glutamicum</i>	
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Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln	
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Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg	
35 40 45	
Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly	
50 55 60	
Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala	
65 70 75 80	
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala	
85 90 95	
Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser	
100 105 110	
Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala	
115 120 125	
Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr	
130 135 140	
Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr	

145 150 155 160
 Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
 165 170 175
 Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
 180 185 190
 Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
 195 200 205
 Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
 210 215 220
 Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
 225 230 235 240
 Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe
 245 250 255
 Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser
 260 265 270
 Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
 275 280 285
 Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
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 Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
 305 310 315 320

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 <213> *Corynebacterium glutamicum*

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 <222> (1)..(762)
 <223> FRXA01180

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 Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
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 tac gcg cta ttt atc gtg toc cgt ttc cgc aat gag ttg att tct cag 96
 Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
 20 25 30

 act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc 144
 Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
 35 40 45

 acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc 192
 Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly

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act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct			240
Thr Ala Gly Ser Ala Val Phe Ala Gly Thr Val Leu Ile Ala			
65	70	75	80
ctg gtt gct ctg tgc atc att aat att cca ttt cta acc gtg atg gcc			288
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala			
	85	90	95
att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc			336
Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser			
	100	105	110
ttc ctg cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca			384
Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala			
	115	120	125
cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg			432
Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr			
	130	135	140
atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac			480
Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr			
	145	150	155
ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc			528
Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr			
	165	170	175
aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc			576
Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr			
	180	185	190
gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc			624
Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly			
	195	200	205
cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag			672
Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu			
	210	215	220
gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac			720
Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn			
	225	230	235
act gat ggt gtg aag aat gct cag atc act cag acc acg gag			762
Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu			
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Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln			

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20 25 30
 Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
 35 40 45
 Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
 50 55 60
 Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
 65 70 75 80
 Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
 85 90 95
 Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
 100 105 110
 Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
 115 120 125
 Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
 130 135 140
 Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
 145 150 155 160
 Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
 165 170 175
 Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
 180 185 190
 Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
 195 200 205
 Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
 210 215 220
 Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
 225 230 235 240
 Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu
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 <213> Corynebacterium glutamicum

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 <223> RXA02586

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 gatgccacca tcatccgcgt gctgcttctc ccccgccgctg atg cac ctg ctt cgc 115
 Met His Leu Leu Arg
 1 5

gac gac aac tgg tgg gca ccc ggc ttc gtt aaa aag gcc tac acc gtc 163
 Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys Lys Ala Tyr Thr Val
 10 15 20

atg ggt cac ggc tct gag gtg gag gaa gca cct cgc cca acc acc cgt 211
 Met Gly His Gly Ser Glu Val Glu Glu Ala Pro Arg Pro Thr Thr Arg
 25 30 35

cgc ctc aac gac gat gag gaa gtc acc gtg cat gaa gca gtt gtc gct 259
 Arg Leu Asn Asp Asp Glu Glu Val Thr Val His Glu Ala Val Val Ala
 40 45 50

ggc gat acc gtg gca tct cgc ggt ggt ttg agc acg cag gaa aac cgt 307
 Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser Thr Gln Glu Asn Arg
 55 60 65

gat ctg gtg tcc ttc gtg gaa ctt aag gct cgt ttg gaa aag cgc agg 355
 Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg Leu Glu Lys Arg Arg
 70 75 80 85

ctt gag gat cta gat taaatctatg cgaggatttt tca 393
 Leu Glu Asp Leu Asp
 90

<210> 224

<211> 90

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

Met His Leu Leu Arg Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys
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Lys Ala Tyr Thr Val Met Gly His Gly Ser Glu Val Glu Glu Ala Pro
 20 25 30

Arg Pro Thr Thr Arg Arg Leu Asn Asp Asp Glu Glu Val Thr Val His
 35 40 45

Glu Ala Val Val Ala Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser
 50 55 60

Thr Gln Glu Asn Arg Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg
 65 70 75 80

Leu Glu Lys Arg Arg Leu Glu Asp Leu Asp
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<212> DNA

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<223> RXA02587

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				Val	Phe	Ser	Lys	Trp	5									
ggc	cac	ttt	gct	tac	aga	ttt	agg	cgc	att	ggt	cgg	tta	gtc	gtc	atc	163		
Gly	His	Phe	Ala	Tyr	Arg	Phe	Arg	Arg	Ile	Val	Pro	Leu	Val	Val	Ile	20		
gcc	gcg	att	ttg	gct	ttg	ttt	gtc	att	ttc	ggc	acc	aag	ctg	ggc	gac	211		
Ala	Ala	Ile	Leu	Ala	Leu	Phe	Val	Ile	Phe	Gly	Thr	Lys	Leu	Gly	Asp	35		
cgc	atg	agc	cag	gaa	gga	tgg	gat	gat	cct	ggt	tct	tcc	tcg	acc	gct	259		
Arg	Met	Ser	Gln	Glu	Gly	Trp	Asp	Asp	Pro	Gly	Ser	Ser	Ser	Thr	Ala	40		
gcg	gcg	cgc	atc	gag	ttg	gag	acc	ttt	ggg	cgt	gac	aat	gac	ggc	gat	307		
Ala	Ala	Arg	Ile	Glu	Leu	Glu	Thr	Phe	Gly	Arg	Asp	Asn	Asp	Gly	Asp	55		
gtc	gtg	ttg	ctg	ttt	act	gcg	cct	gaa	ggc	act	tct	ttc	gat	gat	gca	355		
Val	Val	Leu	Leu	Phe	Thr	Ala	Pro	Glu	Gly	Thr	Ser	Phe	Asp	Asp	Ala	70		
gag	gtg	ttc	tcc	agc	atc	tct	ggc	tac	tta	gat	ggg	cta	atc	gag	aac	403		
Glu	Val	Phe	Ser	Ser	Ile	Ser	Gly	Tyr	Leu	Asp	Gly	Leu	Ile	Glu	Asn	90		
aac	cct	gat	gaa	gtc	agc	cac	atc	aac	agc	tac	ttt	gac	act	cgt	aat	451		
Asn	Pro	Asp	Glu	Val	Ser	His	Ile	Asn	Ser	Tyr	Phe	Asp	Thr	Arg	Asn	105		
caa	aat	ctc	ctc	agc	aaa	gac	ggc	acc	caa	acc	ttt	gca	gct	ctc	ggg	499		
Gln	Asn	Leu	Leu	Ser	Lys	Asp	Gly	Thr	Gln	Thr	Phe	Ala	Ala	Leu	Gly	120		
ctc	aaa	ggt	gac	ggc	gag	caa	acg	ctg	aag	gac	ttc	cgg	gag	att	gaa	547		
Leu	Lys	Gly	Asp	Gly	Glu	Gln	Thr	Leu	Lys	Asp	Phe	Arg	Glu	Ile	Glu	135		
gat	cag	ctc	cat	ccg	gac	aac	ctt	gcc	ggt	ggc	gtc	acc	act	gag	gtc	595		
Asp	Gln	Leu	His	Pro	Asp	Asn	Leu	Ala	Gly	Gly	Val	Thr	Thr	Glu	Val	150		
gcg	ggt	gcc	acc	gct	gta	gcc	gac	gca	ctc	gat	gag	ggc	atg	gct	ggc	643		
Ala	Gly	Ala	Thr	Ala	Val	Ala	Asp	Ala	Leu	Asp	Glu	Gly	Met	Ala	Gly	170		
gat	att	tca	cgc	gcc	gaa	gtt	ttt	gcg	ctg	cct	ttc	gtg	gct	atc	ttg	691		
Asp	Ile	Ser	Arg	Ala	Glu	Val	Phe	Ala	Leu	Pro	Phe	Val	Ala	Ile	Leu	185		
ctg	ctc	atc	gtg	ttt	ggc	tca	gtt	ggt	gcc	gcg	gcg	atg	cca	ttg	atc	739		
Leu	Leu	Ile	Val	Phe	Gly	Ser	Val	Val	Ala	Ala	Ala	Met	Pro	Leu	Ile	200		
gtg	ggc	att	ttg	tcc	atc	ttg	ggt	tcg	ctg	ggc	atc	ttg	gca	att	ttg	787		
Val	Gly	Ile	Leu	Ser	Ile	Leu	Gly	Ser	Leu	Gly	Ile	Leu	Ala	Ile	Leu			

215				220				225								
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ctg Leu	ggc Gly	ttg Leu	ggt Gly	ctt Leu	gcc Ala	att Ile	gac Asp	tat Tyr	ggc Gly	tta Leu	ttc Phe	atg Met	gtc Val	tct Ser	cgt Arg	883
ttc Phe	cgt Arg	gag Glu	gaa Glu	atg Met	gat Asp	aag Lys	ggc Gly	acc Thr	ccg Pro	gtt Val	gaa Glu	cag Gln	gct Ala	gtt Val	gcc Ala	931
acc Thr	act Thr	acg Thr	gcg Ala	acc Thr	gcg Ala	ggg Gly	aag Lys	act Thr	gtg Val	gtg Val	ttc Phe	tct Ser	gca Ala	gcg Ala	atg Met	979
gtg Val	gct Ala	gtg Val	gcg Ala	ctg Leu	tcc Ser	ggg Gly	ttg Leu	ttt Phe	gtt Val	ttc Phe	cca Pro	cag Gln	gct Ala	ttc Phe	ttg Leu	1027
aag Lys	tcg Ser	gtg Val	gca Ala	ttc Phe	ggt Gly	gcg Ala	att Ile	tcc Ser	gcg Ala	gtt Val	ggc Gly	ctt Leu	gct Ala	gct Ala	ttg Leu	1075
atg Met	tcg Ser	gtg Val	acg Thr	gtg Val	ttg Leu	ccg Pro	tcg Ser	ctg Leu	ttc Phe	agc Ser	atg Met	ttg Leu	ggt Gly	aag Lys	aat Asn	1123
atc Ile	gat Asp	aag Lys	tggt Trp	agt Ser	ttg Leu	cgt Arg	cgc Arg	act Thr	gct Ala	cga Ala	aca Thr	gcg Ala	cgc Arg	cgt Arg	ttg Leu	1171
gaa Glu	gac Asp	acc Thr	att Ile	tggt Trp	tac Tyr	cgc Arg	gtg Val	ccg Pro	gca Ala	tggt Trp	gca Ala	atg Met	cgc Arg	cat His	gcc Ala	1219
aag Lys	gca Ala	gtg Val	acc Thr	gtg Val	ggc Gly	gtc Val	gta Val	ttg Leu	ctc Leu	ttg Leu	ctt Leu	gct Ala	ctt Leu	aca Thr	gtg Val	1267
ccg Pro	ttg Leu	acg Thr	ggc Gly	gtg Val	aaa Lys	ttc Phe	ggc Gly	ggc Gly	atc Ile	aat Asn	gaa Glu	acg Thr	tat Tyr	ctg Leu	cca Pro	1315
cca Pro	gct Ala	aac Asn	gac Asp	acc Arg	cgc Arg	gtc Val	gcc Ala	caa Gln	gag Glu	cgt Arg	ttc Phe	gac Asp	gag Glu	gcg Ala	ttt Phe	1363
ccc Pro	gcc Ala	ttc Phe	cgc Arg	acc Thr	gag Glu	ccg Pro	gtc Val	aag Lys	ctt Leu	gtg Val	gtc Val	acc Thr	ggg Gly	gcg Ala	gac Asp	1411
aac Asn	aac Asn	cag Gln	ctg Leu	atc Ile	gat Asp	atc Ile	tat Tyr	gtt Val	cag Gln	gcc Ala	aac Asn	gaa Glu	gtt Val	gag Glu	gga Gly	1459
ctg Leu	aca Thr	gat Asp	cgt Arg	ttc Phe	acc Thr	gca Ala	ggt Gly	gcg Ala	act Thr	acc Thr	gat Asp	gat Asp	ggc Gly	acc Thr	acg Thr	1507

gtg Val 470	tgt Leu	tct Ser	act Thr	ggt Gly	att Ile 475	cag Gln	gat Asp	cgt Arg	tcc Ser	ctc Leu 480	aat Asn	gag Glu	cag Gln	gta Val	gtg Val 485	1555
gag Glu	cag Gln	ctt Leu	cgc Arg	gct Ala 490	att Ile	tcc Ser	gtc Val	cct Pro	gag Glu 495	ggc Gly	gtt Val	gag Glu	gtg Val	cag Gln 500	atc Ile	1603
ggt Gly	ggc Gly	act Thr	cca Pro 505	gcc Ala	atg Met	gag Glu	atc Ile	gaa Glu 510	tcc Ser	att Ile	gag Glu	gcg Ala	ctc Leu 515	ttt Phe	gaa Glu	1651
aag Lys	ctc Leu	ctc Leu 520	tgg Trp	atg Met	gct Ala	ctc Leu	tac Tyr 525	att Ile	gtg Val	ctg Leu	gcc Ala	act Thr 530	ttc Phe	atc Ile	ctc Leu	1699
atg Met	gca Ala 535	ttg Leu	gta Val	ttt Phe	ggt Gly	tcg Val 540	gtg Val	att Ile	ttg Leu	ccg Pro	gcg Ala 545	aag Lys	gcc Ala	atc Ile	atc Ile	1747
atg 550	acc Thr	att Ile	ctg Leu	ggt Gly 555	atg Met	ggt Gly	gcc Ala	acc Thr	ttg Leu 560	ggt Gly	att Ile	ctc Leu	acc Thr	ttg Leu 565	atg Met	1795
ttc Phe	gtc Val	gat Asp	ggc Gly	gtg Val 570	ggt Gly	gcc Ala	agc Ser	gca Ala	ttg Leu 575	aac Asn	ttc Phe	tcc Ser	cct Pro	ggc Gly 580	cca Pro	1843
ctg Leu	atg Met	agt Ser	cca Pro 585	gtg Val	ctg Leu	gtg Val	ctg Leu	atc Ile 590	atg Met	gct Ala	att Ile	att Ile	tac Tyr 595	gga Gly	ctt Leu	1891
tcc Ser	acc Thr	gac Asp 600	tat Tyr	gag Glu	gtg Val	ttc Phe	ctg Leu	gta Val 605	tct Ser	cgc Arg	atg Met 610	gtg Val	gag Glu	gcc Ala	cgc Arg	1939
gat Asp 615	aaa Lys	ggc Gly	gaa Glu	tcc Ser	acc Thr 620	gac Asp	gac Asp	gcc Ala	atc Ile	aga Arg	tac Tyr 625	ggc Gly	act Thr	gca Ala	cac His	1987
acc 630	gga Thr	tct Gly	atc Ser	atc Ile	acc Thr 635	gcg Ala	gcc Ala	gca Ala	ctg Leu	atc Ile 640	atg Met	att Ile	gtg Val	gtc Val	tgt Gly 645	2035
gga Gly	gcg Ala	ttt Phe	ggt Gly	ttc Phe 650	tct Ser	gag Glu	atc Ile	gtc Val	atg Met 655	atg Met	aag Lys	tac Tyr	atc Ile	gcg Ala 660	ttc Phe	2083
ggc Gly	atg Met	atc Ile	gca Ala 665	gcg Ala	ctg Leu	att Ile	ctg Leu	gat Asp 670	gcc Ala	acc Thr	atc Ile	atc Ile	cgc Arg 675	atg Met	ctg Leu	2131
ctt Leu	gtc Val	ccc Pro 680	cgc Arg	cgt Arg	gat Asp	gca Ala	cct Pro 685	gct Pro	tcg Ser	cga Arg	cga Arg	caa Gln 690	ctg Leu	gtg Val	ggc Gly	2179
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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Thr Lys Leu Gly Asp Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly
 35 40 45
 Ser Ser Thr Ala Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg
 50 55 60
 Asp Asn Asp Gly Asp Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr
 65 70 75 80
 Ser Phe Asp Asp Ala Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp
 85 90 95
 Gly Leu Ile Glu Asn Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr
 100 105 110
 Phe Asp Thr Arg Asn Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr
 115 120 125
 Phe Ala Ala Leu Gly Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp
 130 135 140
 Phe Arg Glu Ile Glu Asp Gln Leu His Pro Asp Asn Leu Ala Gly Gly
 145 150 155 160
 Val Thr Thr Glu Val Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp
 165 170 175
 Glu Gly Met Ala Gly Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro
 180 185 190
 Phe Val Ala Ile Leu Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala
 195 200 205
 Ala Met Pro Leu Ile Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly
 210 215 220
 Ile Leu Ala Ile Leu Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln
 225 230 235 240
 Ser Val Val Thr Leu Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu
 245 250 255
 Phe Met Val Ser Arg Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val
 260 265 270
 Glu Gln Ala Val Ala Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val
 275 280 285

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Phe Ser Ala Ala Met Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe
 290 295 300
 Pro Gln Ala Phe Leu Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val
 305 310 315 320
 Gly Leu Ala Ala Leu Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser
 325 330 335
 Met Leu Gly Lys Asn Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg
 340 345 350
 Thr Ala Arg Arg Leu Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp
 355 360 365
 Ala Met Arg His Ala Lys Ala Val Thr Val Gly Val Val Leu Leu Leu
 370 375 380
 Leu Ala Leu Thr Val Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn
 385 390 395 400
 Glu Thr Tyr Leu Pro Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg
 405 410 415
 Phe Asp Glu Ala Phe Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val
 420 425 430
 Val Thr Gly Ala Asp Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala
 435 440 445
 Asn Glu Val Glu Gly Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr
 450 455 460
 Asp Asp Gly Thr Thr Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu
 465 470 475 480
 Asn Glu Gln Val Val Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly
 485 490 495
 Val Glu Val Gln Ile Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile
 500 505 510
 Glu Ala Leu Phe Glu Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu
 515 520 525
 Ala Thr Phe Ile Leu Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro
 530 535 540
 Ala Lys Ala Ile Ile Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly
 545 550 555 560
 Ile Leu Thr Leu Met Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn
 565 570 575
 Phe Ser Pro Gly Pro Leu Met Ser Pro Val Leu Val Leu Ile Met Ala
 580 585 590
 Ile Ile Tyr Gly Leu Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg
 595 600 605
 Met Val Glu Ala Arg Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg

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610 615 620

Tyr Gly Thr Ala His Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile
625 630 635 640

Met Ile Val Val Cys Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met
645 650 655

Lys Tyr Ile Ala Phe Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr
660 665 670

Ile Ile Arg Met Leu Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg
675 680 685

Arg Gln Leu Val Gly Thr Arg Leu Arg
690 695

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<223> RXN03042

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Leu Val Leu Ala Phe
1 5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163
Leu Val Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
10 15 20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
25 30 35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
40 45 50

ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg 307
Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu
55 60 65

gcc atg gat tac cag atc ttc cto gtt act cgt atg cgt gag ggc ttc 355
Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe
70 75 80 85

acc aag ggc aag act gcg ggc aac gca acg tcg aat ggt ttc aag cac 403
Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His
90 95 100

ggt gcc cgc gtg gtc act gct gcg gcg ctg atc atg gtg tct gtg ttc 451
Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe

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gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg 547
 Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met
 135 140 145

att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta 595
 Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu
 150 155 160 165

cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag 643
 Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu
 170 175 180

ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat 691
 Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn
 185 190 195

gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta 729
 Val Gly Val Gly Ala
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<210> 230

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 230

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Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
 35 40 45

Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly
 50 55 60

Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg
 65 70 75 80

Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser
 85 90 95

Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile
 100 105 110

Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile
 115 120 125

Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe
 130 135 140

Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp
 145 150 155 160

Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val
 165 170 175

Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu

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180 185 190

Glu Leu Lys Glu Asn Val Gly Val Gly Ala
195 200

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<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(1582)
<223> RXA01616

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gagttgtaac tgtaccgacc attcgttaca gttacgatcc atg act tca gaa acc 115
Met Thr Ser Glu Thr
1 5

tta cag gcg caa gcg cct acg aaa acc caa cgt tgg gct ttc ctc gcc 163
Leu Gln Ala Gln Ala Pro Thr Lys Thr Gln Arg Trp Ala Phe Leu Ala
10 15 20

gtt atc agc ggt ggt ctc ttt ctg atc ggt gta gac aac tgg att ctc 211
Val Ile Ser Gly Gly Leu Phe Leu Ile Gly Val Asp Asn Ser Ile Leu
25 30 35

tac acc gca ctc cct ctg ctg cgt gaa cag ctc gca gcc tcc gaa acc 259
Tyr Thr Ala Leu Pro Leu Leu Arg Glu Gln Leu Ala Ala Ser Glu Thr
40 45 50

caa gcg ttg tgg atc atc aac gca tat ccc ctg ctc atg gcg ggc ctt 307
Gln Ala Leu Trp Ile Ile Asn Ala Tyr Pro Leu Leu Met Ala Gly Leu
55 60 65

cgt ttg ggt gcc ggc act ttg ggt gac aaa aac ggc cac cgc cgg atg 355
Arg Leu Gly Ala Gly Thr Leu Gly Asp Lys Asn Gly His Arg Arg Met
70 75 80 85

ttc ctc atg ggc ttg agc att ttc gga atc gct tca ctt ggt gct gcg 403
Phe Leu Met Gly Leu Ser Ile Phe Gly Ile Ala Ser Leu Gly Ala Ala
90 95 100

ttt gct cca act gcg tgg gct ctt gtt gct gcg aga gct ttc ctt ggc 451
Phe Ala Pro Thr Ala Trp Ala Leu Val Ala Ala Arg Ala Phe Leu Gly
105 110 115

atc ggt gcg gca acg atg atg cct gca acc ttg gct ctg atc cgc att 499
Ile Gly Ala Ala Thr Met Met Pro Ala Thr Leu Ala Leu Ile Arg Ile
120 125 130

acg ttt gag gat gag cgt gag cgc aac act gca att ggt att tgg ggt 547
Thr Phe Glu Asp Glu Arg Glu Arg Asn Thr Ala Ile Gly Ile Trp Gly
135 140 145

tcc gtg gca att ctt ggc gct gcg gca ggc ccg atc att ggt ggt gcg 595
Ser Val Ala Ile Leu Gly Ala Ala Ala Gly Pro Ile Ile Gly Gly Ala

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150	155	160	165	
ctg ttg gaa ttc ttc tgg tgg ggt tgc gtt ttc ctc att aac gtt ccg				643
Leu Leu Glu Phe Phe Trp Trp Gly Ser Val Phe Leu Ile Asn Val Pro	170	175	180	
gtg gct gtt atc gcg ttg atc gct acg ctt ttt gtg gcg ccg gcc aat				691
Val Ala Val Ile Ala Leu Ile Ala Thr Leu Phe Val Ala Pro Ala Asn	185	190	195	
atc gcg aat ccg tct aag cat tgg gat ttc ttg tgc tgc ttc tat gcg				739
Ile Ala Asn Pro Ser Lys His Trp Asp Phe Leu Ser Ser Phe Tyr Ala	200	205	210	
ctg ctc aca ctt gct ggg ttg atc atc acg atc aag gaa tct gtg aat				787
Leu Leu Thr Leu Ala Gly Leu Ile Ile Thr Ile Lys Glu Ser Val Asn	215	220	225	
act gca cgc cat atg cct ctt ctt ttg ggt gca gtc atc atg ttg atc				835
Thr Ala Arg His Met Pro Leu Leu Leu Gly Ala Val Ile Met Leu Ile	230	235	240	245
att ggt gcg gtg ttg ttt agc agt cgt cag aag aag atc gag gag cca				883
Ile Gly Ala Val Leu Phe Ser Ser Arg Gln Lys Lys Ile Glu Glu Pro	250	255	260	
ctt cta gat ctg tgc ttg ttc cgt aat cgc ctt ttc tta ggc ggt gtg				931
Leu Leu Asp Leu Ser Leu Phe Arg Asn Arg Leu Phe Leu Gly Gly Val	265	270	275	
gtt gct gcg gcc atg gcg atg ttt act gtg tcc ggt ttg gaa atg act				979
Val Ala Ala Gly Met Ala Met Phe Thr Val Ser Gly Leu Glu Met Thr	280	285	290	
acc tgc cag cgt ttc cag ttg tct gtg ggt ttc act cca ctt gag gct				1027
Thr Ser Gln Arg Phe Gln Leu Ser Val Gly Phe Thr Pro Leu Glu Ala	295	300	305	
ggt ttg ctc atg atc cca gct gca ttg ggt agc ttc ccg atg tct att				1075
Gly Leu Leu Met Ile Pro Ala Ala Leu Gly Ser Phe Pro Met Ser Ile	310	315	320	325
atc ggt ggt gca aac ctg cat cgt tgg ggc ttc aaa ccg ctg atc agt				1123
Ile Gly Gly Ala Asn Leu His Arg Trp Gly Phe Lys Pro Leu Ile Ser	330	335	340	
ggt ggt ttt gct gcc act gcc gtt ggc atc gcc ctg tgt att tgg ggc				1171
Gly Gly Phe Ala Ala Thr Ala Val Gly Ile Ala Leu Cys Ile Trp Gly	345	350	355	
gcg act cat act gat ggt ttg ccg ttt ttc atc gcg ggt cta ttc ttc				1219
Ala Thr His Thr Asp Gly Leu Pro Phe Phe Ile Ala Gly Leu Phe Phe	360	365	370	
atg ggc gcg ggt gct ggt tgc gta atg tct gtg tct tcc act gcg att				1267
Met Gly Ala Gly Ala Gly Ser Val Met Ser Val Ser Ser Thr Ala Ile	375	380	385	
atc ggt tcc gcg ccg gtg cgt aag gct ggc atg gcg tgc tgc atc gaa				1315
Ile Gly Ser Ala Pro Val Arg Lys Ala Gly Met Ala Ser Ser Ile Glu	390	395	400	405

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0950203-05300

Ile Gly Ile Trp Gly Ser Val Ala Ile Leu Gly Ala Ala Ala Gly Pro
 145 150 155 160
 Ile Ile Gly Gly Ala Leu Leu Glu Phe Phe Trp Trp Gly Ser Val Phe
 165 170 175
 Leu Ile Asn Val Pro Val Ala Val Ile Ala Leu Ile Ala Thr Leu Phe
 180 185 190
 Val Ala Pro Ala Asn Ile Ala Asn Pro Ser Lys His Trp Asp Phe Leu
 195 200 205
 Ser Ser Phe Tyr Ala Leu Leu Thr Leu Ala Gly Leu Ile Ile Thr Ile
 210 215 220
 Lys Glu Ser Val Asn Thr Ala Arg His Met Pro Leu Leu Leu Gly Ala
 225 230 235 240
 Val Ile Met Leu Ile Ile Gly Ala Val Leu Phe Ser Ser Arg Gln Lys
 245 250 255
 Lys Ile Glu Glu Pro Leu Leu Asp Leu Ser Leu Phe Arg Asn Arg Leu
 260 265 270
 Phe Leu Gly Gly Val Val Ala Ala Gly Met Ala Met Phe Thr Val Ser
 275 280 285
 Gly Leu Glu Met Thr Thr Ser Gln Arg Phe Gln Leu Ser Val Gly Phe
 290 295 300
 Thr Pro Leu Glu Ala Gly Leu Leu Met Ile Pro Ala Ala Leu Gly Ser
 305 310 315 320
 Phe Pro Met Ser Ile Ile Gly Gly Ala Asn Leu His Arg Trp Gly Phe
 325 330 335
 Lys Pro Leu Ile Ser Gly Gly Phe Ala Ala Thr Ala Val Gly Ile Ala
 340 345 350
 Leu Cys Ile Trp Gly Ala Thr His Thr Asp Gly Leu Pro Phe Phe Ile
 355 360 365
 Ala Gly Leu Phe Phe Met Gly Ala Gly Ala Gly Ser Val Met Ser Val
 370 375 380
 Ser Ser Thr Ala Ile Ile Gly Ser Ala Pro Val Arg Lys Ala Gly Met
 385 390 395 400
 Ala Ser Ser Ile Glu Glu Val Ser Tyr Glu Phe Gly Thr Leu Leu Ser
 405 410 415
 Val Ala Ile Leu Gly Ser Leu Phe Pro Phe Phe Tyr Ser Leu His Ala
 420 425 430
 Pro Ala Glu Val Ala Asp Asn Phe Ser Ala Gly Val His His Ala Ile
 435 440 445
 Asp Gly Asp Ala Ala Arg Ala Ser Leu Asp Thr Ala Tyr Ile Asn Val
 450 455 460
 Leu Ile Ile Ala Leu Val Cys Ala Val Ala Ala Ala Leu Ile Ser Ser

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0960308 0157300

150	155	160	165
ttc ttg ggc atg gaa atc acc ctg tgg atc tgc ctt ggg ctc tca ctt Phe Leu Gly Met Glu Ile Thr Leu Trp Ile Cys Leu Gly Leu Ser Leu	170	175	180
gtc gcg ctg ctg cac ctg ctg ccg att cgc gtc gac gaa ccg gaa atc Val Ala Leu Leu His Leu Leu Pro Ile Arg Val Asp Glu Pro Glu Ile	185	190	195
atc acc caa gaa gac gca cag cct act gtt tct gac gat tca gtt ccc Ile Thr Gln Glu Asp Ala Gln Pro Thr Val Ser Asp Ser Val Pro	200	205	210
aca cct acc tcc gat ttg gcg atc gtg tcc aaa ggc atc gac cta aaa Thr Pro Thr Ser Asp Leu Ala Ile Val Ser Lys Gly Ile Asp Leu Lys	215	220	225
gga tca atg aaa atc atc ctg agt gtt ccg gga ctg ctc gcg ctt gtg Gly Ser Met Lys Ile Ile Leu Ser Val Pro Gly Leu Leu Ala Leu Val	230	235	240
ttg ttt gcg tcc ttc aac aac ctc atc ggc ggc gtg tac tcc gca ctc Leu Phe Ala Ser Phe Asn Asn Leu Ile Gly Gly Val Tyr Ser Ala Leu	250	255	260
atg gac cct tac ggc ctg gaa ctt ttc agc cca cag ctg tgg ggg cta Met Asp Pro Tyr Gly Leu Glu Leu Phe Ser Pro Gln Leu Trp Gly Leu	265	270	275
ctg ctt gga ctc acc agc ctc ggc ttc atc gtt ggt ggt gct gtg atc Leu Leu Gly Leu Thr Ser Leu Gly Phe Ile Val Gly Gly Ala Val Ile	280	285	290
tcc aaa act ggc ttg ggc aaa aac cct gtg cgc acc ttg ctg ctg gtt Ser Lys Thr Gly Leu Gly Lys Asn Pro Val Arg Thr Leu Leu Leu Val	295	300	305
aat gtt ggt gtg gct ttt gtt ggc atg tta ttt gcc att cgc gaa tgg Asn Val Gly Val Ala Phe Val Gly Met Leu Phe Ala Ile Arg Glu Trp	310	315	320
tgg tgg ctc tac atc ctg ggc att ttc atc ttc atg gct atc acc cca Trp Trp Leu Tyr Ile Leu Gly Ile Phe Ile Phe Met Ala Ile Thr Pro	330	335	340
gct gcc gaa gcc gca gaa caa acc atc ctt caa cga gtc gtc cca ttc Ala Ala Glu Ala Ala Glu Gln Thr Ile Leu Gln Arg Val Val Pro Phe	345	350	355
cgc caa caa ggc cgc gta ttt gga cta gcc atg gca gtg gaa atg gca Arg Gln Gln Gly Arg Val Phe Gly Leu Ala Met Ala Val Glu Met Ala	360	365	370
gcc aac ccg ctc tcc aca gtg atc gtg gcg att ttg gcc gaa gcc tac Ala Asn Pro Leu Ser Thr Val Ile Val Ala Ile Leu Ala Glu Ala Tyr	375	380	385
ctc att cca tgg atg gct ggc ccc ggc gcg gac acc atc tgg ggc gtg Leu Ile Pro Trp Met Ala Gly Pro Gly Ala Asp Thr Ile Trp Gly Val	390	395	400
			405

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atc ctc ggc gag ggt aaa gct cgc ggc atg gca ctg atg ttc ctc gca 1363
 Ile Leu Gly Glu Gly Lys Ala Arg Gly Met Ala Leu Met Phe Leu Ala
 410 415 420

tca ggt gcc atc atg ttg gtt gtc gtg ctg ttg gca ttc atg tcg agg 1411
 Ser Gly Ala Ile Met Leu Val Val Val Leu Leu Ala Phe Met Ser Arg
 425 430 435

tcc tac cgg aaa ctc agc cag tac tac gcc acc acc agc caa gac att 1459
 Ser Tyr Arg Lys Leu Ser Gln Tyr Tyr Ala Thr Thr Ser Gln Asp Ile
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gcg gga gct gct gag aag taagtgtct agaccgttgt ttg 1500
 Ala Gly Ala Ala Glu Lys
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<210> 234

<211> 459

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 234

Val Ser Thr Phe His Lys Val Leu Ile Asn Thr Met Ile Ser Asn Val
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Thr Thr Gly Phe Leu Phe Phe Ala Val Val Phe Trp Met Tyr Leu Ser
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Thr Gly Asn Val Ala Leu Thr Gly Ile Val Ser Gly Ile Tyr Met Gly
 35 40 45

Leu Ile Ala Val Cys Ser Ile Phe Phe Gly Thr Val Val Asp His Asn
 50 55 60

Arg Lys Lys Ser Val Met Leu Phe Ser Ser Val Thr Thr Leu Val Phe
 65 70 75 80

Tyr Cys Leu Ser Ala Leu Val Trp Val Phe Trp Leu Glu Glu Asp Gly
 85 90 95

Leu Ser Ile Gly Asn Thr Ala Leu Trp Val Phe Val Ser Phe Ile Leu
 100 105 110

Ile Gly Ser Ile Val Glu His Met Arg Asn Ile Ala Leu Ser Thr Val
 115 120 125

Val Thr Leu Leu Val Pro Glu Ala Glu Arg Asp Lys Ala Asn Gly Leu
 130 135 140

Val Gly Ala Val Gln Gly Val Gly Phe Leu Val Thr Ser Val Ile Ala
 145 150 155 160

Gly Ser Ala Ile Gly Phe Leu Gly Met Glu Ile Thr Leu Trp Ile Cys
 165 170 175

Leu Gly Leu Ser Leu Val Ala Leu Leu His Leu Leu Pro Ile Arg Val
 180 185 190

Asp Glu Pro Glu Ile Ile Thr Gln Glu Asp Ala Gln Pro Thr Val Ser

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      195              200              205
Asp Asp Ser Val Pro Thr Pro Thr Ser Asp Leu Ala Ile Val Ser Lys
 210              215              220
Gly Ile Asp Leu Lys Gly Ser Met Lys Ile Ile Leu Ser Val Pro Gly
 225              230              235
Leu Leu Ala Leu Val Leu Phe Ala Ser Phe Asn Asn Leu Ile Gly Gly
      245              250              255
Val Tyr Ser Ala Leu Met Asp Pro Tyr Gly Leu Glu Leu Phe Ser Pro
 260              265              270
Gln Leu Trp Gly Leu Leu Leu Gly Leu Thr Ser Leu Gly Phe Ile Val
 275              280              285
Gly Gly Ala Val Ile Ser Lys Thr Gly Leu Gly Lys Asn Pro Val Arg
 290              295              300
Thr Leu Leu Leu Val Asn Val Gly Val Ala Phe Val Gly Met Leu Phe
 305              310              315
Ala Ile Arg Glu Trp Trp Trp Leu Tyr Ile Leu Gly Ile Phe Ile Phe
 325              330              335
Met Ala Ile Thr Pro Ala Ala Glu Ala Ala Glu Gln Thr Ile Leu Gln
 340              345              350
Arg Val Val Pro Phe Arg Gln Gln Gly Arg Val Phe Gly Leu Ala Met
 355              360              365
Ala Val Glu Met Ala Ala Asn Pro Leu Ser Thr Val Ile Val Ala Ile
 370              375              380
Leu Ala Glu Ala Tyr Leu Ile Pro Trp Met Ala Gly Pro Gly Ala Asp
 385              390              395
Thr Ile Trp Gly Val Ile Leu Gly Glu Gly Lys Ala Arg Gly Met Ala
 405              410              415
Leu Met Phe Leu Ala Ser Gly Ala Ile Met Leu Val Val Val Leu Leu
 420              425              430
Ala Phe Met Ser Arg Ser Tyr Arg Lys Leu Ser Gln Tyr Tyr Ala Thr
 435              440              445
Thr Ser Gln Asp Ile Ala Gly Ala Ala Glu Lys
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<210> 235

<211> 1521

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1498)

<223> RXA00062

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Phe	Ile	Trp	Phe	Leu	Arg	His	Glu	Ser	Ser	Ala	Lys	Glu	Pro	Leu	Leu	
230					235					240				245		
ccc	ctg	ggg	ctc	ttt	aaa	aac	cgc	agg	cga	aac	acc	atc	ttg	gcc	agc	883
Pro	Leu	Gly	Leu	Phe	Lys	Asn	Arg	Arg	Arg	Asn	Thr	Ile	Leu	Ala	Ser	
				250					255					260		
cgc	ttt	ctt	ctg	gtt	ggc	tcc	gtg	atg	tca	ttc	ttc	ttc	ttt	gcc	acc	931
Arg	Phe	Leu	Val	Gly	Ser	Val	Met	Met	Ser	Phe	Phe	Phe	Phe	Ala	Thr	
				265				270					275			
cag	ctg	ttc	cag	gac	acc	atg	gga	atg	aat	gct	ctc	cag	gca	ggc	ctt	979
Gln	Leu	Phe	Gln	Asp	Thr	Met	Gly	Met	Asn	Ala	Leu	Gln	Ala	Gly	Leu	
				280				285				290				
gcg	ttc	atg	ccg	cta	tct	ctg	ctg	cag	ttt	gcc	agc	gcc	gcg	atg	gtg	1027
Ala	Phe	Met	Pro	Leu	Ser	Leu	Leu	Gln	Phe	Ala	Ser	Ala	Ala	Met	Val	
				295			300				305					
cca	cgg	ctt	tcc	cga	gca	ggc	gta	tct	gat	tcc	atg	ctc	acc	gtc	atc	1075
Pro	Arg	Leu	Ser	Arg	Ala	Gly	Val	Ser	Asp	Ser	Met	Leu	Thr	Val	Ile	
310				315						320				325		
ggt	ttc	gcc	atc	atg	gtc	atc	ggc	atg	gca	ggc	ctc	gca	ttt	gta	cca	1123
Gly	Phe	Ala	Ile	Met	Val	Ile	Gly	Met	Ala	Gly	Leu	Ala	Phe	Val	Pro	
				330					335					340		
aac	acg	atg	atc	gcg	ctg	atc	cta	cca	ata	ggt	ttg	gtg	gga	ttt	ggc	1171
Asn	Thr	Met	Ile	Ala	Leu	Ile	Leu	Pro	Ile	Val	Leu	Val	Gly	Phe	Gly	
				345				350					355			
caa	ggc	ttc	gct	ttc	gga	cca	atg	aca	gct	ctg	gca	ggt	caa	ggt	gca	1219
Gln	Gly	Phe	Ala	Phe	Gly	Pro	Met	Thr	Ala	Leu	Ala	Val	Gln	Gly	Ala	
				360			365					370				
ccg	aag	gac	caa	tcc	ggc	gcc	gtt	tct	ggc	ctg	gtg	aat	tcc	ctt	cac	1267
Pro	Lys	Asp	Gln	Ser	Gly	Ala	Val	Ser	Gly	Leu	Val	Asn	Ser	Leu	His	
				375		380					385					
caa	atc	ggc	ggc	acc	ttc	ggt	ttg	ggt	gtg	ttc	tcc	tcc	ttg	gct	gtc	1315
Gln	Ile	Gly	Gly	Thr	Phe	Gly	Leu	Gly	Val	Phe	Ser	Ser	Leu	Ala	Val	
390				395					400					405		
gct	gtc	atc	gga	cat	gat	gca	aca	tca	gag	atg	atc	agc	gac	cgc	gca	1363
Ala	Val	Ile	Gly	His	Asp	Ala	Thr	Ser	Glu	Met	Ile	Ser	Asp	Arg	Ala	
				410					415					420		
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cagcatccca gtt

1521

<210> 236

<211> 466

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

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Ile Asp Pro Val His Leu Ser Trp Val Gln Ser Ser Tyr Thr Leu Val
 35 40 45

Phe Gly Ala Leu Leu Leu Leu Gly Ala Arg Ala Gly Asp Ile Phe Gly
 50 55 60

Arg Lys Lys Val Leu Tyr Ile Gly Leu Ala Leu Phe Ala Ala Ser Ser
 65 70 75 80

Leu Ala Ile Ala Leu Ser Pro Asn Ala Ala Val Leu Ile Gly Ala Arg
 85 90 95

Val Val Gln Gly Ala Gly Ala Ala Ile Ile Ala Pro Ala Thr Leu Ala
 100 105 110

Leu Ile Thr Glu Phe Phe Pro Glu Gly Pro Ala Arg Leu Arg Ala Thr
 115 120 125

Ser Ala Tyr Gly Ala Val Ala Gly Ile Gly Val Ala Ala Gly Leu Val
 130 135 140

Ile Gly Gly Val Phe Ala Asp Leu Leu Ser Trp Arg Ile Gly Phe Phe
 145 150 155 160

Ile Asn Val Pro Ile Ala Ala Val Leu Ala Tyr Ile Val His Lys Ala
 165 170 175

Ile Pro Ala Thr Phe Ser Arg Pro Gly Ser Leu Asp Ile Phe Gly Ala
 180 185 190

Ile Thr Ser Thr Ala Gly Ile Ala Ala Val Leu Tyr Ala Ile Val Arg
 195 200 205

Ser Ala Asp Tyr Ser Trp Thr Asp Pro Phe Val Leu Ile Ser Leu Val
 210 215 220

Leu Gly Ile Ala Val Phe Ile Trp Phe Leu Arg His Glu Ser Ser Ala
 225 230 235 240

Lys Glu Pro Leu Leu Pro Leu Gly Leu Phe Lys Asn Arg Arg Arg Asn
 245 250 255

Thr Ile Leu Ala Ser Arg Phe Leu Leu Val Gly Ser Val Met Ser Phe
 260 265 270

00660200-066300

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 Leu Gln Ala Gly Leu Ala Phe Met Pro Leu Ser Leu Leu Gln Phe Ala
 290 295 300
 Ser Ala Ala Met Val Pro Arg Leu Ser Arg Ala Gly Val Ser Asp Ser
 305 310 315 320
 Met Leu Thr Val Ile Gly Phe Ala Ile Met Val Ile Gly Met Ala Gly
 325 330 335
 Leu Ala Phe Val Pro Asn Thr Met Ile Ala Leu Ile Leu Pro Ile Val
 340 345 350
 Leu Val Gly Phe Gly Gln Gly Phe Ala Phe Gly Pro Met Thr Ala Leu
 355 360 365
 Ala Val Gln Gly Ala Pro Lys Asp Gln Ser Gly Ala Val Ser Gly Leu
 370 375 380
 Val Asn Ser Leu His Gln Ile Gly Gly Thr Phe Gly Leu Gly Val Phe
 385 390 395 400
 Ser Ser Leu Ala Val Ala Val Ile Gly His Asp Ala Thr Ser Glu Met
 405 410 415
 Ile Ser Asp Arg Ala His Phe Gly Phe Leu Leu Ser Thr Val Thr Leu
 420 425 430
 Thr Leu Ala Thr Ile Phe Ala Val Thr Leu Leu Lys Arg His Glu Thr
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 Arg Lys Ser Ser Glu Arg Pro Thr Gln Leu Val Asp Glu Lys Ala Val
 450 455 460
 Thr Ser
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<210> 237

<211> 1584

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1561)

<223> RXA00215

<400> 237

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 Val Ser Asp Lys Lys 5
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cag gat cta aca tcc tcc gca gca ggt agt gct gca ccc caa acc aag 163
 Gln Asp Leu Thr Ser Ser Ala Ala Gly Ser Ala Ala Pro Gln Thr Lys 20
 10 15

00603208-062300

09603208 = 051300

Phe Ala Trp Phe Ile Tyr Gln Gln Ser Arg Ala Glu Lys Ser Gly Asn
 265 270 275
 gat cct ctc gtc cca ctg gag att ttc aag ttt aga aac ttc agc ctc 979
 Asp Pro Leu Val Pro Leu Glu Ile Phe Lys Phe Arg Asn Phe Ser Leu
 280 285 290
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 Gly Asn Ile Cys Ile Met Ala Met Gly Phe Thr Val Ala Gly Thr Pro
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 ctg ccc atc atg ttg tac ttc cag caa gca cac gga atg aac gcc atg 1075
 Leu Pro Ile Met Leu Tyr Phe Phe Gln Gln Ala His Gly Met Asn Ala Met
 310 315 320 325
 gaa gcg ggt ttc atg atg gtg cct caa gct ctc atg gca gca gta ctg 1123
 Glu Ala Gly Phe Met Met Val Pro Gln Asp Leu Met Ala Ala Val Leu
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 Ser Pro Phe Val Gly Lys Leu Val Asp Arg Ser Asn Pro Gly Leu Met
 345 350 355
 gca gcc ctc ggt ttt agc aca gtg gct gtg tcc att gta ctg ctg tca 1219
 Ala Ala Leu Gly Phe Ser Thr Val Ala Val Ser Ile Val Leu Leu Ser
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 atg gta atg att ttc gat acg ggt cta gtc tgg gca ctt gtt tcg atg 1267
 Met Val Met Ile Phe Asp Thr Gly Leu Val Trp Ala Leu Val Ser Met
 375 380 385
 act ttg ctc ggc atc gga aac gcc ttt gtg tgg gca ccg aac tcg acc 1315
 Thr Leu Leu Gly Ile Gly Asn Ala Phe Val Trp Ala Pro Asn Ser Thr
 390 395 400 405
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 Ser Thr Met Arg Asp Leu Pro His Lys Phe Met Gly Ala Gly Ser Gly
 410 415 420
 gtg ttc aat aca acc cgc caa tta ggt tca gtc atc ggc gcc gct gcc 1411
 Val Phe Asn Thr Thr Arg Gln Leu Gly Ser Val Ile Gly Ala Ala Ala
 425 430 435
 atc ggc gcg gta atg cag att cga ctg gca gca gcc gat gag gcc gca 1459
 Ile Gly Ala Val Met Gln Ile Arg Leu Ala Ala Gly Asp Glu Gly Ala
 440 445 450
 gct ttt ggt caa gca ctt cta ctt gcc gct gcg gtg ctg gtt atc gcc 1507
 Ala Phe Gly Gln Ala Leu Leu Ala Ala Val Leu Val Ile Gly
 455 460 465
 att gtg gca tca acg atg gca gga aaa aat gca cac cca gcg ccg gta 1555
 Ile Val Ala Ser Thr Met Ala Gly Lys Asn Ala His Pro Ala Pro Val
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 Lys Pro

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 238

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 35 40 45

Leu Asp Gln Thr Ile Val Ala Val Ser Thr Pro Ala Leu Gln Ala Asp
 50 55 60

Met Gly Ala Ser Tyr Asn Glu Val Ile Trp Val Thr Ser Val Tyr Leu
 65 70 75 80

Leu Thr Phe Ala Val Pro Leu Leu Val Thr Gly Arg Leu Gly Asp Lys
 85 90 95

Tyr Gly Pro Lys Asn Val Tyr Val Ala Gly Met Val Ile Phe Thr Val
 100 105 110

Ser Ser Leu Ala Cys Gly Leu Ala Pro Asp Met Phe Thr Leu Ile Ile
 115 120 125

Ala Arg Gly Val Gln Gly Leu Gly Ala Ala Leu Leu Thr Pro Gln Thr
 130 135 140

Met Ala Thr Ile Asn Arg Ile Phe Ala Phe Glu Arg Arg Gly Ala Ala
 145 150 155 160

Leu Gly Val Trp Gly Ser Thr Ala Gly Leu Ala Ser Leu Ala Gly Pro
 165 170 175

Ile Leu Gly Gly Val Ile Thr Glu Asn Trp Gly Trp Gln Trp Val Phe
 180 185 190

Tyr Ile Asn Val Pro Ile Gly Val Ile Ser Val Ile Ala Val Met Lys
 195 200 205

Tyr Val Pro Glu Phe Pro Pro Leu Thr Arg Pro Leu Asp Pro Leu Ser
 210 215 220

Ile Val Leu Ser Ile Val Ala Val Phe Phe Leu Val Phe Ala Phe Gln
 225 230 235 240

Glu Gly Glu Gly Ala Gly Trp Ala Ala Trp Val Trp Ile Met Ile Val
 245 250 255

Ala Ala Phe Ala Leu Phe Ala Trp Phe Ile Tyr Gln Gln Ser Arg Ala
 260 265 270

Glu Lys Ser Gly Asn Asp Pro Leu Val Pro Leu Glu Ile Phe Lys Phe
 275 280 285

Arg Asn Phe Ser Leu Gly Asn Ile Cys Ile Met Ala Met Gly Phe Thr
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002200-002200

Val Ala Gly Thr Pro Leu Pro Ile Met Leu Tyr Phe Gln Gln Ala His
305 310 315 320

Gly Met Asn Ala Met Glu Ala Gly Phe Met Met Val Pro Gln Ala Leu
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340 345 350

Asn Pro Gly Leu Met Ala Ala Leu Gly Phe Ser Thr Val Ala Val Ser
355 360 365

Ile Val Leu Leu Ser Met Val Met Ile Phe Asp Thr Gly Leu Val Trp
370 375 380

Ala Leu Val Ser Met Thr Leu Leu Gly Ile Gly Asn Ala Phe Val Trp
385 390 395 400

Ala Pro Asn Ser Thr Ser Thr Met Arg Asp Leu Pro His Lys Phe Met
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Gly Ala Gly Ser Gly Val Phe Asn Thr Thr Arg Gln Leu Gly Ser Val
420 425 430

Ile Gly Ala Ala Ala Ile Gly Ala Val Met Gln Ile Arg Leu Ala Ala
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Gly Asp Glu Gly Ala Ala Phe Gly Gln Ala Leu Leu Leu Ala Ala Ala
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His Pro Ala Pro Val Lys Pro
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<211> 1455

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1432)

<223> RXN03064

<400> 239

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Met Met Leu Asn Glu
1 5

act act ctg gca gtc gcg ttg ccg tgc atc atg gcg gac ttt gac att 163
Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met Ala Asp Phe Asp Ile
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gag gcg aat act gcg cag tgg ttg ctc act ggt ttt atg ttg acc atg 211
Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly Phe Met Leu Thr Met

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cgt agt gtg ttt att ttc gcc acg gtg gtc ttc ctg atc ggt act gtg			307
Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe Leu Ile Gly Thr Val			
55	60	65	
acg gct gcg ttg tct cct act ttt gcg att atg ctt gca gcc cgc gtc			355
Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met Leu Ala Ala Arg Val			
70	75	80	85
gct cag gcg att ggt acc gct gtg atc atg ccg ctg ctg atg act gtc			403
Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro Leu Leu Met Thr Val			
90	95	100	
gcg atg acc gtt gtt cct cca gag cgc cgt ggc gcc gtc atg ggt ttg			451
Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly Ala Val Met Gly Leu			
105	110	115	
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Ile Ala Val Val Met Ala Val Gly Pro Ala Leu Gly Pro Ser Val Ala			
120	125	130	
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Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala Ile Phe Trp Val Met			
135	140	145	
gtt ccg ttg gtg ttt gtg gca agc ctg atc ggt acc ctg cgt ctg acc			595
Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly Thr Leu Arg Leu Thr			
150	155	160	165
aac gtc agt gag cct aaa aag act cct ttg gat gtt att tcc ttc ctg			643
Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp Val Ile Ser Phe Leu			
170	175	180	
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Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr Ala Leu Ser Ser Ile			
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ggc atc att ttg gaa ggt gac aga agc gct ttg gtc gtg ttg gct gtc			739
Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu Val Val Leu Ala Val			
200	205	210	
ggc atc att gcg ttg gtg gtg ttt gtg tgg cgc cag att gcc atg ggt			787
Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg Gln Ile Ala Met Gly			
215	220	225	
aag cag gat aag gcg ctg ttg gat ctg cgt ccg ttg gcg att cgt gag			835
Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro Leu Ala Ile Arg Glu			
230	235	240	245
tac acc att ccg ctg gtt gtg ctt ttg acg ctg ttc ggt gcg ctg ctc			883
Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu Phe Gly Ala Leu Leu			
250	255	260	
ggt gtc atg aat aca ctg ccg ctc tac ctg cag gga tcc ttg atg gtc			931
Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln Gly Ser Leu Met Val			
265	270	275	

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acc gcc ttg gtc gcg ggt cta gtg ctg ttg cca ggt ggt ctt ttg gaa 979
 Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro Gly Gly Leu Leu Glu
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ggg gtg ctg tgg cca ttt ggt ggt cga att tat gat cgt cat ggt cca 1027
 Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr Asp Arg His Gly Pro
 295 300 305

cgc gga ctc gtg atc ggc ggt atg tca ctc gtt gtg atc tcc ctg ttt 1075
 Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val Ile Ser Leu Phe
 310 315 320 325

gca ctg tcc acc gtc gat gag ttc gcc aac gtg tgg ttc atc atc ggc 1123
 Ala Leu Ser Thr Val Asp Glu Phe Ala Asn Val Trp Phe Ile Ile Gly
 330 335 340

gta cac atc gtg ttc tcc atc ggc ctt gcg ctg ctg ttc acc cca ctg 1171
 Val His Ile Val Phe Ser Ile Gly Leu Ala Leu Leu Phe Thr Pro Leu
 345 350 355

atg aca gtc gcg ctc gca tcc gtc ccc gac aac atg tac ggc cac ggc 1219
 Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn Met Tyr Gly His Gly
 360 365 370

tcc gcg atc ctc aac acc ctc caa cag ctc gcc ggc gcc gca ggc acc 1267
 Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala Gly Ala Ala Gly Thr
 375 380 385

gcg gtc atg att gcg gtt tat tcc acc gtc agc aac aac gcg ctt atc 1315
 Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser Asn Asn Ala Leu Ile
 390 395 400 405

gac ggc gca acc caa caa acc gcc ctc gcc gac ggc gcc aac tct gca 1363
 Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp Gly Ala Asn Ser Ala
 410 415 420

ttc ttc gcc tca gcg tgc gtg gca gtg ttt gca ctg atc gtg ggc ttc 1411
 Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala Leu Ile Val Gly Phe
 425 430 435

ttt gta aag agg cca gcc cgc taagctaggt cgcgatgatca gca 1455
 Phe Val Lys Arg Pro Ala Arg
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<210> 240
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 240
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Ala Asp Phe Asp Ile Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly
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Phe Met Leu Thr Met Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu
 35 40 45

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0660303 055300

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370                               375                               380
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Asn Asn Ala Leu Ile Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp
405                               410                               415
Gly Ala Asn Ser Ala Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala
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Leu Ile Val Gly Phe Phe Val Lys Arg Pro Ala Arg
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<213> Corynebacterium glutamicum

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Met Met Leu Asn Glu
1 5
act act ctg gca gtc gcg ttg ccg tgg atc atg gcg gac ttt gac att 163
Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met Ala Asp Phe Asp Ile
10 15 20
gag gcg aat act gcg cag tgg ttg ctc act ggt ttt atg ttg acc atg 211
Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly Phe Met Leu Thr Met
25 30 35
gct gtg gtt ctt cca gct act ggt tgg atg ttg gaa cgt ttt acc act 259
Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu Glu Arg Phe Thr Thr
40 45 50
cgt agt gtg ttt att ttc gcc acg gtg gtc ttc ctg atc ggt act gtg 307
Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe Leu Ile Gly Thr Val
55 60 65
acg gct gcg ttg tct cct act ttt gcg att atg ctt gca gcc cgc gtc 355
Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met Leu Ala Ala Arg Val
70 75 80 85
gct cag gcg att ggt acc gct gtg atc atg ccg ctg ctg atg act gtc 403
Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro Leu Leu Met Thr Val
90 95 100
gcg atg acc gtt gtt cct cca gag cgc cgt ggc gcc gtc atg ggt ttg 451
Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly Ala Val Met Gly Leu
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09603078

<211> 331

<213> Cor

<400> 242

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Phe Met Leu Thr Met Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu
 35 40 45

Glu Arg Phe Thr Thr Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe
 50 55 60

Leu Ile Gly Thr Val Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met
 65 70 75 80

Leu Ala Ala Arg Val Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro
 85 90 95

Leu Leu Met Thr Val Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly
 100 105 110

Ala Val Met Gly Leu Ile Ala Val Val Met Ala Val Gly Pro Ala Leu
 115 120 125

Gly Pro Ser Val Ala Gly Phe Val Leu Ser Leu Ser Trp His Ala
 130 135 140

Ile Phe Trp Val Met Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly
 145 150 155 160

Thr Leu Arg Leu Thr Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp
 165 170 175

Val Ile Ser Phe Leu Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr
 180 185 190

Ala Leu Ser Ser Ile Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu
 195 200 205

Val Val Leu Ala Val Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg
 210 215 220

Gln Ile Ala Met Gly Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro
 225 230 235 240

Leu Ala Ile Arg Glu Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu
 245 250 255

Phe Gly Ala Leu Leu Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln
 260 265 270

Gly Ser Leu Met Val Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro
 275 280 285

Gly Gly Leu Leu Glu Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr
 290 295 300

Asp Arg His Gly Pro Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val
 305 310 315 320

002200-002300

Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn Met Tyr Gly His Gly

35 40 45

Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala Gly Ala Ala Gly Thr
50 55 60

Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser Asn Asn Ala Leu Ile
65 70 75 80

Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp Gly Ala Asn Ser Ala
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Phe Val Lys Arg Pro Ala Arg
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<223> RXA00648

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Val Val Thr Leu Ala
1 5

tca gct ggt atc act gtt tcc cta gcg cag acc ctg gtt att ccg atc 163
Ser Ala Gly Ile Thr Val Ser Leu Ala Gln Thr Leu Val Ile Pro Ile
10 15 20

att ggt cgg ttg ccc gag atc ttc aac acc acg gct gct aat gcc tct 211
Ile Gly Arg Leu Pro Glu Ile Phe Asn Thr Thr Ala Ala Asn Ala Ser
25 30 35

tgg atc att act gtg acg ctg ttg gtg ggc gca gtg gcg act cct gtg 259
Trp Ile Ile Thr Val Thr Leu Leu Val Gly Ala Val Ala Thr Pro Val
40 45 50

atg ggc agg ctt gca gat atg tac ggc aag aaa aag atg atg ctc atc 307
Met Gly Arg Leu Ala Asp Met Tyr Gly Lys Lys Lys Met Met Leu Ile
55 60 65

tca ctt gtc ccg ttc att ctt gga tca gtg atc tgc gct gtg tcg gtg 355
Ser Leu Val Pro Phe Ile Leu Gly Ser Val Ile Cys Ala Val Ser Val
70 75 80 85

gat ttg att ccg atg atc atc ggc cgt ggt ttt cag ggg ctt ggc tct 403
Asp Leu Ile Pro Met Ile Ile Gly Arg Gly Phe Gln Gly Leu Gly Ser
90 95 100

ggc ctg att cct ctt ggc att tct ctc atg cat gat ttg ttg ccc cgg 451
Gly Leu Ile Pro Leu Gly Ile Ser Leu Met His Asp Leu Leu Pro Arg

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agt ggc ggc ttt gat tat ttc ggt gct ctc ggc ctt gca atg gga ctt Ser Gly Gly Phe Asp Tyr Phe Gly Ala Leu Gly Leu Trp Gly Leu 185 190 195			691
atc gca ttg ttg ctc gcg gtg tcc aag gga tca gaa tgg ggc tgg aga Ile Ala Leu Leu Leu Ala Val Ser Lys Gly Ser Glu Trp Gly Trp Arg 200 205 210			739
agt gcc ctg acc att ggg tta ttc gtg gca gcg ctg gtg att ttg gtg Ser Ala Leu Thr Ile Gly Leu Phe Val Ala Ala Leu Val Ile Leu Val 215 220 225			787
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cgc acc act att cgg gcg acc gtg ttg atg aca aat att gcg tcc atc Arg Thr Thr Ile Arg Ala Thr Val Leu Met Thr Asn Ile Ala Ser Ile 250 255 260			883
ctc atc ggt ttc acc atg tat gga atg aat ctg atc ctg cct cag gtc Leu Ile Gly Phe Thr Met Tyr Gly Met Asn Leu Ile Leu Pro Gln Val 265 270 275			931
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00602200 0022300

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Asn Ala Leu Ile Leu Thr Thr Leu Val Leu Phe Ser Val Cys Ser Leu	
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gtg gtc ggt atc ggc att ggc ctg gca ttt ggt tcc atg cct gcc ttg	1267
Val Val Gly Ile Gly Ile Gly Leu Ala Phe Gly Ser Met Pro Ala Leu	
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atc atg ggt gcc gta cca gcc acg gag aaa gcc gca gcg aat ggt ttc	1315
Ile Met Gly Ala Val Pro Ala Thr Glu Lys Ala Ala Ala Asn Gly Phe	
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aac tct ctt atg cgt tca ctg ggc acc acc ggc tca tca gct gtc atc	1363
Asn Ser Leu Met Arg Ser Leu Gly Thr Thr Gly Ser Ser Ala Val Ile	
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415	
420	
ggc gca gtg ttg gcc gga atg atg agt ggc gga gta ccc acc tta ggg	1411
Gly Ala Val Leu Ala Gly Met Met Ser Gly Gly Val Pro Thr Leu Gly	
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435	
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Gly Phe Met Thr Thr Leu Ile Ile Gly Cys Cys Ala Ala Leu Val Ala	
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Lys	
470	
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Val Ala Thr Pro Val Met Gly Arg Leu Ala Asp Met Tyr Gly Lys Lys	
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Gln Gly Leu Gly Ser Gly Leu Ile Pro Leu Gly Ile Ser Leu Met His	
100 105 110	

Asp Leu Leu Pro Arg Glu Lys Ala Gly Ser Ala Ile Ala Leu Met Ser
 115 120 125
 Ser Ser Met Gly Ile Gly Gly Ala Leu Gly Leu Pro Leu Ala Ala Ala
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 Ile Ala Gln Phe Ala Ser Trp Arg Val Leu Phe Trp Phe Thr Ala Leu
 145 150 155 160
 Val Ala Leu Thr Val Gly Ala Val Ile Trp Lys Ala Ile Pro Ala Arg
 165 170 175
 Pro Arg Ile Val Arg Ser Gly Gly Phe Asp Tyr Phe Gly Ala Leu Gly
 180 185 190
 Leu Ala Met Gly Leu Ile Ala Leu Leu Leu Ala Val Ser Lys Gly Ser
 195 200 205
 Glu Trp Gly Trp Arg Ser Ala Leu Thr Ile Gly Leu Phe Val Ala Ala
 210 215 220
 Leu Val Ile Leu Val Gly Trp Gly Trp Phe Glu Thr Arg Gln Lys Ser
 225 230 235 240
 Pro Leu Ile Asp Leu Arg Thr Thr Ile Arg Ala Thr Val Leu Met Thr
 245 250 255
 Asn Ile Ala Ser Ile Leu Ile Gly Phe Thr Met Tyr Gly Met Asn Leu
 260 265 270
 Ile Leu Pro Gln Val Met Gln Leu Pro Val Ile Leu Gly Tyr Gly Leu
 275 280 285
 Gly Gln Ser Met Leu Gln Met Gly Ile Trp Leu Ile Pro Met Gly Leu
 290 295 300
 Gly Met Met Leu Ile Ser Asn Ala Gly Ala Ala Ile Ser Ala Ala His
 305 310 315 320
 Gly Pro Arg Val Thr Leu Thr Ile Ala Gly Val Val Ile Ala Val Gly
 325 330 335
 Tyr Ala Leu Thr Ala Thr Val Leu Phe Thr Ile Gly Asn Arg Thr Pro
 340 345 350
 Gly Gly Asp Ala Asp Asn Ala Leu Ile Leu Thr Thr Leu Val Leu Phe
 355 360 365
 Ser Val Cys Ser Leu Val Val Gly Ile Gly Ile Gly Leu Ala Phe Gly
 370 375 380
 Ser Met Pro Ala Leu Ile Met Gly Ala Val Pro Ala Thr Glu Lys Ala
 385 390 395 400
 Ala Ala Asn Gly Phe Asn Ser Leu Met Arg Ser Leu Gly Thr Thr Gly
 405 410 415
 Ser Ser Ala Val Ile Gly Ala Val Leu Ala Gly Met Met Ser Gly Gly
 420 425 430
 Val Pro Thr Leu Gly Gly Phe Met Thr Thr Leu Ile Ile Gly Cys Cys

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aag ccg gac gac gaa cgt ccg gta aca aca att tca aaa agt ggt gca 163 Lys Pro Asp Asp Glu Arg Pro Val Thr Thr Ile Ser Lys Ser Gly Ala 20																	
cct tcg gcc cac acc tca gca cca tat ggt gca gca gca act gaa gaa 211 Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala Ala Ala Thr Glu Glu 35																	
gct gtc gag gaa aaa acc aaa ggt cgc gtt gga ttt atc atc gca gcc 259 Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly Phe Ile Ile Ala Ala 50																	
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cag aac atg acc acc ttg att gtg gct cgt gca ctg cag ggt atc gcc 547 Gln Asn Met His Thr Leu Ile Val Ala Arg Ala Leu Gln Gly Ile Ala 145																	

056030

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acc gcc cgt gag cgt gca aag tac atg ggc atc atg ggt tcc gtt ttc Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile Met Gly Ser Val Phe 170 175 180	643
gga ctg tcc tcc atc ctt ggc cca ttg ctt ggt ggc tgg ttc act gac Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Asp 185 190 195	691
ggt cca ggc tgg cgt tgg ggt ctg tgg ttg aac gtt cca atc ggc atc Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn Val Pro Ile Gly Ile 200 205 210	739
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gcc acc acc gca ttt gtc ctc gca gtg acc tgg ggt ggc aat gaa tat Ala Thr Thr Ala Phe Val Leu Ala Val Thr Trp Gly Gly Asn Glu Tyr 250 255 260	883
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 Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr Phe Phe Val Phe
 390 395 400 405

gga ttc ggc ctg ggc tgt gca atg cag att ttg gtt ctc atc gtg cag 1363
 Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val Leu Ile Val Gln
 410 415 420

aac tcc ttc cca atc acc atg gtt ggc acc gcg acc ggt tcc aac aac 1411
 Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala Thr Gly Ser Asn Asn
 425 430 435

ttc ttc cgc caa atc ggt gga gca gta ggt tcc gca ctg atc ggt ggc 1459
 Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala Leu Ile Gly Gly
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 Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu Asn Val Pro Ala
 455 460 465

gca gtg gct tcc atg ggt gaa gaa ggc gca caa tac gcc tca gca atg 1555
 Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr Ala Ser Ala Met
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tcc gat ttc tcc ggt gca tcc aac ctc act cca cac ctt gtt gaa tca 1603
 Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His Leu Val Glu Ser
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 Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu Ser Tyr Asn Asp Ala
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 520 525 530

atc ctc ctc ttt ttc atc cgt gaa gat cac ctc aag gaa acg cac gaa 1747
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<213> Corynebacterium glutamicum

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Ala Ala Thr Glu Glu Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly
 35 40 45

Phe Ile Ile Ala Ala Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly
 50 55 60

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Gln Thr Ile Phe Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly
 65 70 75 80
 Gly Val Asn His Met Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln
 85 90 95
 Thr Ile Ser Leu Pro Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg
 100 105 110
 Lys Tyr Leu Phe Met Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile
 115 120 125
 Ile Gly Ala Leu Ala Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala
 130 135 140
 Leu Gln Gly Ile Ala Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile
 145 150 155 160
 Thr Ala Asp Val Thr Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile
 165 170 175
 Met Gly Ser Val Phe Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly
 180 185 190
 Gly Trp Phe Thr Asp Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn
 195 200 205
 Val Pro Ile Gly Ile Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys
 210 215 220
 Leu Pro Ala Arg Glu Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser
 225 230 235 240
 Ile Phe Met Ala Ile Ala Thr Thr Ala Phe Val Leu Ala Val Thr Trp
 245 250 255
 Gly Gly Asn Glu Tyr Glu Trp Ala Ser Pro Met Ile Ile Gly Leu Phe
 260 265 270
 Ile Thr Thr Leu Val Ala Ala Ile Val Phe Val Phe Val Glu Lys Arg
 275 280 285
 Ala Val Asp Pro Leu Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe
 290 295 300
 Val Leu Thr Ala Val Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly
 305 310 315 320
 Thr Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn
 325 330 335
 Pro Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile
 340 345 350
 Gly Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr
 355 360 365
 Lys Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val
 370 375 380
 Leu Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu

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0963708 : 06300

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Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asn His Met
70 75 80 85

acc tgg gtg att acc gcc ttc ctc ttg ggc cag acc att tca ttg cct 403
Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln Thr Ile Ser Leu Pro
90 95 100

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Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg Lys Tyr Leu Phe Met
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Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile Ile Gly Ala Leu Ala
120 125 130

cag aac atg acc acc ttg att gtg gct cgt gca ctg cag ggt atc gcc 547
Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala Leu Gln Gly Ile Ala
135 140 145

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Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Thr Ala Asp Val Thr
150 155 160 165

acc gcc cgt gag cgt gca aag tac atg ggc atc atg ggt tcc gtt ttc 643
Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile Met Gly Ser Val Phe
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Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Asp
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200 205 210

atc gca ctg gtt gct atc gct gtg ctg ctg aaa ctt cca gct cgt gaa 787
Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys Leu Pro Ala Arg Glu
215 220 225

cgt ggc aag gtc tcc gtt gac tgg ttg gga agc atc ttc atg gct atc 835
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<212> PRT

<213> Corynebacterium glutamicum

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Leu Thr Ala Tyr Met Pro Thr Tyr	20	25	30	
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Ile Ala Tyr Met Pro Thr Tyr	35	40	45	
acg caa gct ggt ctg atg ctg atc cca atg atg atc ggc ctg att ggt				192
Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met	50	55	60	
aca tcc act gtg gtg ggc aac atc gtg tcc aag act ggc aag tac aag				240
Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys	65	70	75	80
tgg tac cca ttc atc ggc atg ctc atc atg gtc ctt gcc cta gta ctg				288
Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu	85	90	95	
cta tcg acg ctg aca cct tcg gca agc ttg gct ctc att gga ctg tac				336
Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr	100	105	110	
ttc ttc gtc ttc gga ttc ggc ctg ggc tgt gca atg cag att ttg gtt				384
Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val	115	120	125	
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Leu Ile Val Gln Asn Ser Ser Pro Ile Thr Met Val Gly Thr Ala Thr	130	135	140	
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Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala	145	150	155	160
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Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu	165	170	175	
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Asn Val Pro Ala Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr	180	185	190	
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Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His	195	200	205	
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Leu Val Glu Ser Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu Ser	210	215	220	
tac aac gac gcc ctg aca cca atc ttc ttg gcg ctc acc ccg atc gca				720
Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala	225	230	235	240
gta gtc gcc gcg atc ctc ctc ttt ttc atc cgt gaa gat cac ctc aag				768
Val Val Ala Ala Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu Lys	245	250	255	

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803

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 Glu Thr His Glu
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 35 40 45
 Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly
 50 55 60
 Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys
 65 70 75 80
 Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu
 85 90 95
 Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr
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 Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val
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 130 135 140
 Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala
 145 150 155 160
 Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu
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 Asn Val Pro Ala Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr
 180 185 190
 Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His
 195 200 205
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 210 215 220
 Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala
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 Glu Thr His Glu

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260

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 Met Thr His Glu Thr
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 Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala Gly Asp Thr Lys Leu
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 Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser Ala Leu Met Val Ala
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 Met Met Met Ala Ser Leu Asp Gln Met Ile Phe Gly Thr Ala Leu Pro
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 Thr Ile Val Gly Glu Leu Gly Gly Val Asp His Met Met Trp Val Ile
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 Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu Pro Ile Tyr Gly Lys
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Val	Leu	Gly	Pro	Leu	Leu	Gly	Gly	Trp	Phe	Thr	Glu	Gly	Pro	Gly	Trp	
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Val	Ala	Ile	Tyr	Phe	Leu	Thr	Asp	Ile	Pro	Lys	Lys	Ser	Val	Lys	Phe	Arg
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Ile	Ile	Ile	Gly	Leu	Ile	Ile	Thr	Thr	Ile	Val	Ala	Ala	Ala	Leu	Leu	
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Ser	Asn	Thr	Gly	Lys	Tyr	Lys	Leu	Phe	Pro	Pro	Ile	Gly	Met	Val	Val	
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Thr	Phe	Val	Ala	Leu	Ile	Phe	Phe	Ala	Arg	Met	Glu	Val	Ser	Thr	Thr	
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ctg	tgg	cag	atc	gga	atc	tac	ctc	ttc	gtc	ctc	ggc	gtc	ggc	ctg	ggt	1315
Leu	Trp	Gln	Ile	Gly	Ile	Tyr	Leu	Phe	Val	Leu	Gly	Val	Gly	Leu	Gly	
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425																430				
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440																445				
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455																460				
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Ser	Pro	Glu	Glu	Gln	Ala	Ala	Met	Ala	Ala	Gln	Gly	Gly	Leu	Asp	Ser					
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aac	gaa	ttg	acg	ccg	gca	atc	gtc	aat	caa	ttg	cca	acc	gcg	ctc	cac	1603				
Asn	Glu	Leu	Thr	Pro	Ala	Ile	Val	Asn	Gln	Leu	Pro	Thr	Ala	Leu	His					
490																495				
gat	gcg	ttc	gcc	ggt	tcc	tac	aac	gac	gca	ctc	atc	cca	gtg	ttc	tac	1651				
Asp	Ala	Phe	Ala	Gly	Ser	Tyr	Asn	Asp	Ala	Leu	Ile	Pro	Val	Phe	Tyr					
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gtg	atg	atg	cca	ctg	atc	ggc	atc	gcg	ctg	ctt	ctc	ttg	ctg	ttt	att	1699				
Val	Met	Met	Pro	Leu	Ile	Gly	Ile	Ala	Leu	Leu	Leu	Leu	Leu	Phe	Ile					
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aag	caa	gaa	aaa	cta	cgc	gaa	acc	acc	aca	gac	taa	acacacaaa	acaaatgaga	1752						
Lys	Gln	Glu	Lys	Leu	Arg	Glu	Thr	Thr	Thr	Asp										
535																540				
cct																1755				
<p><210> 254</p> <p><211> 544</p> <p><212> PRT</p> <p><213> Corynebacterium glutamicum</p>																				
<p><400> 254</p> <p>Met Thr His Glu Thr Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala</p> <p>1 5 10 15</p> <p>Gly Asp Thr Lys Leu Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro</p> <p>20 25 30</p> <p>Ser Ser Met Thr Pro Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser</p> <p>35 40 45</p> <p>Ala Leu Met Val Ala Met Met Met Ala Ser Leu Asp Gln Met Ile Phe</p> <p>50 55 60</p> <p>Gly Thr Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asp His</p> <p>65 70 75 80</p> <p>Met Met Trp Val Ile Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu</p> <p>85 90 95</p>																				

[illegible]

420					425					430						
Phe	Phe	Arg	Gln	Ile	Gly	Ser	Ser	Leu	Gly	Ser	Ala	Leu	Val	Gly	Gly	
435					440					445						
Met	Phe	Val	Gly	Asn	Leu	Gly	Thr	Leu	Met	Glu	Glu	Arg	Met	Pro	Ala	
450					455					460						
Ala	Met	Ala	Gln	Leu	Ser	Pro	Glu	Glu	Gln	Ala	Ala	Met	Ala	Ala	Gln	
465					470					475					480	
Gly	Gly	Leu	Asp	Ser	Asn	Glu	Leu	Thr	Pro	Ala	Ile	Val	Asn	Gln	Leu	
485					490					495					500	
Pro	Thr	Ala	Leu	His	Asp	Ala	Phe	Ala	Gly	Ser	Tyr	Asn	Asp	Ala	Leu	
500					505					510					515	
Ile	Pro	Val	Phe	Tyr	Val	Met	Met	Pro	Leu	Ile	Gly	Ile	Ala	Leu	Leu	
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ttttcatccg tgaagatcac ctcaaggaaa cgcacgaata atg aca cac gaa act 115
Met Thr His Glu Thr
1 5

tcc gtc ccc gga cct gcc gac gcg cag gtc gca gga gat acg aag ctg 163
Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala Gly Asp Thr Lys Leu
10 15 20

cgc aaa ggc cgc gcg aag aag gaa aaa act cct tca tca atg acg cct 211
Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro Ser Ser Met Thr Pro
25 30 35

gaa caa caa aag aaa gtc tgg tgg gtc ctc agc gcg ctg atg gtc gcc 259
Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser Ala Leu Met Val Ala
40 45 50

atg atg atg gcc tcc ctt gac cag atg att ttc ggc aca gcc ctg cca 307
Met Met Met Ala Ser Leu Asp Gln Met Ile Phe Gly Thr Ala Leu Pro
55 60 65

aca atc qtc qgt qaa ctc ggc ggc gtt gac cac atg atg tgg gtc atc 355

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Thr Ile Val Gly Glu Leu Gly Gly Val Asp His Met Met Trp Val Ile 70 75 80 85	
acc gca tac cta ctt gcc gaa acc atc atg ctg ccg atc tac gga aag Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu Pro Ile Tyr Gly Lys 90 95 100	403
ctc gcc gac ctg gtt gga cgt aaa ggt ctc ttc atc gga gcc ctc gcc Leu Gly Asp Leu Val Gly Arg Lys Ala Leu Gly 105 110 115	451
atc ttc ctg atc gcc tcc gtc atc gcc ggg ctt gca gga aat atg acc Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu Ala Gly Asn Met Thr 120 125 130	499
tgg ttg atc gtc gcc cgt gcc gta cag gcc atc ggt gcc ggt gga ctg Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile Gly Gly Gly Gly Leu 135 140 145	547
atg atc ctc tcg cag gca atc atc gcg gac gtt gtt cca gca cgt gaa Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val Val Pro Ala Arg Glu 150 155 160 165	595
cgt gcc cgc tac atg ggt gtc atg ggt gga gtc ttc gga ctc tct gca Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val Phe Gly Leu Ser Ala 170 175 180	643
gtt ctt gcc cca cta ctc ggt gcc tgg ttc acc gaa gga cca gcc tgg Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Glu Gly Pro Gly Trp 185 190 195	691
cgc tgg gca ttc tgg atg aac atc cca ctg gga atc atc gcc atc ggt Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly Ile Ala Ile Gly 200 205 210	739
gtc gcc att tac ttc ctg gac att cca aag aag agc gtc aag ttc cgc Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys Ser Val Lys Phe Arg 215 220 225	787
tgg gat tac ctg gcc act ttc ttc atg atc gtt gcc gca acc agc ctg Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val Ala Ala Thr Ser Leu 230 235 240 245	835
atc ctg ttc acc acc tgg ggt gga tcc cag tac gag tgg tct gat cca Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr Glu Trp Ser Asp Pro 250 255 260	883
atc atc att gga ctg atc atc acc acc atc gtt gcc gct gca ctg ctg Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val Ala Ala Ala Leu Leu 265 270 275	931
gtt gtt gtg gaa ctg cgc gca aaa gat cca ttg gtt cca atg tcc ttc Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu Val Pro Met Ser Phe 280 285 290	979
ttc caa aac cgc aac ttc acg ctc acc acc att gca gcc ctg atc ctg Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile Ala Gly Leu Ile Leu 295 300 305	1027
ggt atc gca atg ttc gcc atc atc gcc tac ctt ccg acc tac ctc cag Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu Pro Thr Tyr Leu Gln	1075

002390-802390

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atg gtc cac gga atc aac gcc acc gaa gcc ggc tac atg ctg atc cca				1123
Met Val His Gly Ile Asn Ala Thr Glu Ala Gly Tyr Met Leu Ile Pro	330	335	340	
atg atg gtc ggc atg atg ggt acc tcc atc tgg act ggt atc cgc atc				1171
Met Met Val Gly Met Met Gly Thr Ser Ile Trp Thr Gly Ile Arg Ile	345	350	355	
tcc aac aca gga aag tac aaa ctc ttc cca cca atc ggc atg gtg gtt				1219
Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro Ile Gly Met Val Val	360	365	370	
acc ttc gtg gca ctg atc ttc ttt gcc cga atg gaa gtg tcc acc acc				1267
Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met Glu Val Ser Thr Thr	375	380	385	
ctg tgg cag atc gga atc tac ctc ttc				1294
Leu Trp Gln Ile Gly Ile Tyr Leu Phe	390	395		
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<213> <i>Corynebacterium glutamicum</i>				
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Gly Asp Thr Lys Leu Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro	20	25	30	
Ser Ser Met Thr Pro Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser	35	40	45	
Ala Leu Met Val Ala Met Met Met Ala Ser Leu Asp Gln Met Ile Phe	50	55	60	
Gly Thr Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asp His	65	70	75	80
Met Met Trp Val Ile Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu	85	90	95	
Pro Ile Tyr Gly Lys Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe	100	105	110	
Ile Gly Ala Leu Gly Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu	115	120	125	
Ala Gly Asn Met Thr Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile	130	135	140	
Gly Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val	145	150	155	160
Val Pro Ala Arg Glu Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val	165	170	175	

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Phe Gly Leu Ser Ala Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr
 180 185 190
 Glu Gly Pro Gly Trp Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly
 195 200 205
 Ile Ile Ala Ile Gly Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys
 210 215 220
 Ser Val Lys Phe Arg Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val
 225 230 235 240
 Ala Ala Thr Ser Leu Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr
 245 250 255
 Glu Trp Ser Asp Pro Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val
 260 265 270
 Ala Ala Ala Leu Leu Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu
 275 280 285
 Val Pro Met Ser Phe Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile
 290 295 300
 Ala Gly Leu Ile Leu Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu
 305 310 315 320
 Pro Thr Tyr Leu Gln Met Val His Gly Ile Asn Ala Thr Glu Ala Gly
 325 330 335
 Tyr Met Leu Ile Pro Met Met Val Gly Met Met Gly Thr Ser Ile Trp
 340 345 350
 Thr Gly Ile Arg Ile Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro
 355 360 365
 Ile Gly Met Val Val Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met
 370 375 380
 Glu Val Ser Thr Thr Leu Trp Gln Ile Gly Ile Tyr Leu Phe
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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <223> RXA01578

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 Met Ile Ala Leu Leu Val Ala
 1 5

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Tyr Leu Gly Gln Arg Arg Thr Trp Ala Leu Leu Leu Ser Thr Leu Leu
 250 255 260
 aca atg acc ggt gta ttc gcc gta atg aat ggt ctg ctg ccc aac ctt 929
 Thr Met Thr Gly Val Phe Ala Val Met Asn Gly Leu Leu Pro Asn Leu
 265 270
 gcg cag gat gct gcc aac ggt gcc gcc atg tca gcg agc gtg gtg tcc 977
 Ala Gln Asp Ala Ala Asn Gly Ala Gly Met Ser Ala Ser Val Val Ser
 280 285 290 295
 tgg tgg aca ctt acc cca tat gcg ctg gct gcc ttg gta ttc ggt cca 1025
 Trp Trp Thr Leu Thr Pro Tyr Ala Leu Ala Gly Leu Val Phe Gly Pro
 300 305 310
 atc gcc gga att ctc gcc gga aaa ttt gga tac aag atc gtc ctg caa 1073
 Ile Ala Gly Ile Leu Ala Gly Lys Phe Gly Tyr Lys Ile Val Leu Gln
 315 320 325
 att ggt atc gct gcc acc atc atc gcc gtt gcc gga gcc acc ttc tta 1121
 Ile Gly Ile Ala Ala Thr Ile Ile Gly Val Ala Gly Ala Thr Phe Leu
 330 335 340
 gtc gga agc acc tcg cat ctc gcg tac ctc gcc atc tcc atc ttc gtg 1169
 Val Gly Ser Thr Ser His Leu Ala Tyr Leu Gly Ile Ser Ile Phe Val
 345 350 355
 ggt att acc tat gca ggt att gcc aac atc atg ctc aac gcc ctg gcc 1217
 Gly Ile Thr Tyr Ala Gly Ile Ala Asn Ile Met Leu Asn Gly Leu Gly
 360 365 370 375
 atc gtg ctc tcc cct gct aac aac caa gcc tat ctg cct gcc atg aac 1265
 Ile Val Leu Ser Pro Ala Asn Asn Gln Gly Tyr Leu Pro Gly Met Asn
 380 385 390
 gca ggt gcc ttc aac cta ggt gca ggt att tcc ttc gcc atc ctc ttc 1313
 Ala Gly Ala Phe Asn Leu Gly Ala Gly Ile Ser Phe Ala Ile Leu Phe
 395 400 405
 gca gtt tcc acg gca ttc agt gac aac gcc gga gga tac gcc gca gcc 1361
 Ala Val Ser Thr Ala Phe Ser Asp Asn Gly Gly Tyr Tyr Ala Ala Gly
 410 415 420
 atg tgg gct gcc gtg atc atc ttg gtc cta gcc ttc ctc tgc tcc ctg 1409
 Met Trp Ala Gly Val Ile Ile Leu Val Leu Ala Phe Leu Cys Ser Leu
 425 430 435
 ctg atc cca cgc cca gaa tca atc acc gat aca gtg gca gcc aaa gtc 1457
 Leu Ile Pro Arg Pro Glu Ser Ile Thr Asp Thr Val Ala Ala Lys Val
 440 445 450 455
 cag gct gaa gaa gcc gct caa gcc gcc agc taaatccaca aactgaacta 1507
 Gln Ala Glu Glu Ala Ala Gln Ala Ala Ser
 460 465
 agg 1510

<210> 258

<211> 465

<212> PRT

00003200 002300

<213> Corynebacterium glutamicum

<400> 258

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Met Leu Ala Pro Ala Leu Ala Thr Met Glu Thr Glu Leu Asn Ala Thr
 20             25             30

Ala Ala Gln Ile Gly Met Thr Gln Thr Ala Phe Phe Thr Ala Ala Ala
 35             40             45

Leu Phe Ser Leu Phe Leu Pro Arg Trp Gly Asp Leu Ile Gly Arg Arg
 50             55             60

Lys Val Leu Val Gly Met Met Ile Val Thr Gly Ile Gly Cys Val Val
 65             70             75             80

Ala Ala Phe Ala Pro Asn Val Thr Ile Leu Phe Leu Gly Arg Leu Ile
 85             90             95

Gln Gly Val Ala Gly Pro Thr Val Pro Leu Cys Leu Ile Ile Leu Arg
100             105             110

Gln Gln Val Thr Asn Glu Lys Gln Tyr Ala Leu Leu Leu Gly Ile Val
115             120             125

Thr Ser Val Asn Gly Gly Ile Gly Gly Val Asp Ala Leu Ala Gly Gly
130             135             140

Trp Leu Ala Glu Thr Leu Gly Phe Arg Ser Ile Phe Trp Val Met Ala
145             150             155             160

Ala Phe Cys Ala Val Ala Ala Leu Ala Leu Pro Phe Ser Val Lys Glu
165             170             175

Ser Thr Ala Glu Thr Pro Lys Met Asp Trp Leu Gly Val Leu Pro
180             185             190

Leu Ala Val Ser Ile Gly Ser Leu Leu Met Ala Phe Asn Glu Ala Gly
195             200             205

Lys Leu Gly Ala Ala Asn Trp Ile Leu Val Val Val Leu Phe Ile Ile
210             215             220

Gly Ile Ala Gly Val Ile Phe Phe Tyr Asn Ile Glu Lys Arg Val Lys
225             230             235             240

His Pro Leu Val Ser Val Glu Tyr Leu Gly Gln Arg Arg Thr Trp Ala
245             250             255

Leu Leu Leu Ser Thr Leu Leu Thr Met Thr Gly Val Phe Ala Val Met
260             265             270

Asn Gly Leu Leu Pro Asn Leu Ala Gln Asp Ala Ala Asn Gly Ala Gly
275             280             285

Met Ser Ala Ser Val Val Ser Trp Trp Thr Leu Thr Pro Tyr Ala Leu
290             295             300

Ala Gly Leu Val Phe Gly Pro Ile Ala Gly Ile Leu Ala Gly Lys Phe

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ggt gat cgt tat gga cag cga aat att tat ctt gcc ggc atg gct gtg 355
 Gly Asp Arg Tyr Gly Gln Arg Asn Ile Tyr Leu Ala Gly Met Ala Val
 70 75 80 85

ttt acc ctc gcg gcg ttg gcc tgt gta ttt gca cca agc atc gaa tgg 403
 Phe Thr Leu Ala Ala Leu Ala Cys Val Phe Ala Pro Ser Ile Glu Trp
 90 95 100

ttg att gct gct cgc gcg gtg cag gcc ctg gcc gga tct ctt ctt aat 451
 Leu Ile Ala Ala Arg Ala Val Gln Gly Leu Gly Gly Ser Leu Leu Asn
 105 110 115

ccg cag ccc ctg agc atc att cac aag att ttc gcg cat gat cgt agg 499
 Pro Gln Pro Leu Ser Ile Ile His Lys Ile Phe Ala His Asp Arg Arg
 120 125 130

gga gcc gcc acc ggg gtg tgg agt gct gtt gcc tca tca gct gga ctt 547
 Gly Ala Ala Thr Gly Val Trp Ser Ala Val Ala Ser Ser Ala Gly Leu
 135 140 145

ttc ggg cca gtt atc ggt ggt gtt ctg gtg ggg tgg atc agc tgg cgt 595
 Phe Gly Pro Val Ile Gly Gly Val Leu Val Gly Trp Ile Ser Trp Arg
 150 155 160 165

gct gtg ttc ttg gtt tat gtg ccg ctc gga ttg atc tcc cta ttt atg 643
 Ala Val Phe Leu Val Tyr Val Pro Leu Gly Leu Ile Ser Leu Phe Met
 170 175 180

gtg gcg cgt tat gtg cct aaa ctt ccc acg gga acc tcg aag atc gat 691
 Val Ala Arg Tyr Val Pro Lys Leu Pro Thr Gly Thr Ser Lys Ile Asp
 185 190 195

tgg ctc tcg ggt gcg gtc tca ctt gtt gct gta ctt ggt gtg gtt ctt 739
 Trp Leu Ser Gly Ala Val Ser Leu Val Ala Val Leu Gly Val Val Leu
 200 205 210

gcc ttg cag cag ggg cca gaa ctt ggg tgg gga aca ctg att tgg gtg 787
 Ala Leu Gln Gln Gly Pro Glu Leu Gly Trp Gly Thr Leu Ile Trp Val
 215 220 225

tcc ctt gcc gtt ggt att gct gca gct gtg ctc ttt ata tgg atg caa 835
 Ser Leu Ala Val Gly Ile Ala Ala Ala Val Leu Phe Ile Trp Met Gln
 230 235 240 245

aca aga tcc aag gcg cca ctg atg ccg ttg agg att ttc aag acg cgc 883
 Thr Arg Ser Lys Ala Pro Leu Met Pro Leu Arg Ile Phe Lys Thr Arg
 250 255 260

aac ttc gcg atc ggt gca ttt tcg atc ttc agc ctg gcc ttt acg gtg 931
 Asn Phe Ala Ile Gly Ala Phe Ser Ile Phe Ser Leu Gly Phe Thr Val
 265 270 275

tat tcc gtt aat ttg ccc atc atg ttg tat ctg caa acg gct cag gga 979
 Tyr Ser Val Asn Leu Pro Ile Met Leu Tyr Leu Gln Thr Ala Gln Gly
 280 285 290

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 Met Ser Ser Gln Leu Ala Gly Leu Met Leu Val Pro Met Gly Ile Ile
 295 300 305

tct gtg gtg atg tca cca gta att gga cga ttg gtg gat cgc ctg gca 1075
 Ser Val Val Met Ser Pro Val Ile Gly Arg Leu Val Asp Arg Leu Ala
 310 315 320 325

cca gga atg atc tcc aag atc gga ttc ggc gcg ctg att ttc tgc atg 1123
 Pro Gly Met Ile Ser Lys Ile Gly Phe Gly Ala Leu Ile Phe Ser Met
 330 335 340

gcg ttg atg gct gtc ttt atg atc gcc aac cta tgc ccg tgg tgg cta 1171
 Ala Leu Met Ala Val Phe Met Ile Ala Asn Leu Ser Pro Trp Trp Leu
 345 350 355

ctc atc ccg att att ttg ttc ggt agc tcc aac gcg atg agt ttt gca 1219
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 360 365 370

ccg aac tct gtg att gct ctg cgt gat gtt ccg cag gat tta gtg ggc 1267
 Pro Asn Ser Val Ile Ala Leu Arg Asp Val Pro Gln Asp Leu Val Gly
 375 380 385

tct gct tct ggt ttt tac aac acc tca cgc cag gtg ggc gct gtt ttg 1315
 Ser Ala Ser Gly Phe Tyr Asn Thr Ser Arg Gln Val Gly Ala Val Leu
 390 395 400 405

ggc gcc gct acc ttg ggc gct gtg atg caa ata gga gtg ggc acg gtg 1363
 Gly Ala Ala Thr Leu Gly Ala Val Met Gln Ile Gly Val Gly Thr Val
 410 415 420

tcc ttc ggt gtt gcc atg ggt gcg gca atc ctg gtg aca ctc gtg ccc 1411
 Ser Phe Gly Val Ala Met Gly Ala Ala Ile Leu Val Thr Leu Val Pro
 425 430 435

tta atc ttt ggg ttc cta gcg gta acc caa ttt aga tagttgctcc 1457
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 440 445

gattttctca cga 1470

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<211> 449

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 260

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Ser Val Gly Leu Phe Leu Thr Leu Leu Asp Gln Ser Leu Val Ala Val
 20 25 30

Ala Leu Pro Lys Ile Gln Glu Asp Leu Gly Ala Ser Leu Asn Gln Ala
 35 40 45

Val Trp Val Ser Ala Val Tyr Leu Leu Thr Phe Ala Val Pro Leu Leu
 50 55 60

00602008-062300

Ile Thr Gly Arg Leu Gly Asp Arg Tyr Gly Gln Arg Asn Ile Tyr Leu
 65 70 75 80
 Ala Gly Met Ala Val Phe Thr Leu Ala Ala Leu Ala Cys Val Phe Ala
 85 90 95
 Pro Ser Ile Glu Trp Leu Ile Ala Ala Arg Ala Val Gln Gly Leu Gly
 100 105 110
 Gly Ser Leu Leu Asn Pro Gln Pro Leu Ser Ile Ile His Lys Ile Phe
 115 120 125
 Ala His Asp Arg Arg Gly Ala Ala Thr Gly Val Trp Ser Ala Val Ala
 130 135 140
 Ser Ser Ala Gly Leu Phe Gly Pro Val Ile Gly Gly Val Leu Val Gly
 145 150 155 160
 Trp Ile Ser Trp Arg Ala Val Phe Leu Val Tyr Val Pro Leu Gly Leu
 165 170 175
 Ile Ser Leu Phe Met Val Ala Arg Tyr Val Pro Lys Leu Pro Thr Gly
 180 185 190
 Thr Ser Lys Ile Asp Trp Leu Ser Gly Ala Val Ser Leu Val Ala Val
 195 200 205
 Leu Gly Val Val Leu Ala Leu Gln Gln Gly Pro Glu Leu Gly Trp Gly
 210 215 220
 Thr Leu Ile Trp Val Ser Leu Ala Val Gly Ile Ala Ala Val Leu
 225 230 235 240
 Phe Ile Trp Met Gln Thr Arg Ser Lys Ala Pro Leu Met Pro Leu Arg
 245 250 255
 Ile Phe Lys Thr Arg Asn Phe Ala Ile Gly Ala Phe Ser Ile Phe Ser
 260 265 270
 Leu Gly Phe Thr Val Tyr Ser Val Asn Leu Pro Ile Met Leu Tyr Leu
 275 280 285
 Gln Thr Ala Gln Gly Met Ser Ser Gln Leu Ala Gly Leu Met Leu Val
 290 295 300
 Pro Met Gly Ile Ile Ser Val Val Met Ser Pro Val Ile Gly Arg Leu
 305 310 315 320
 Val Asp Arg Leu Ala Pro Gly Met Ile Ser Lys Ile Gly Phe Gly Ala
 325 330 335
 Leu Ile Phe Ser Met Ala Leu Met Ala Val Phe Met Ile Ala Asn Leu
 340 345 350
 Ser Pro Trp Trp Leu Leu Ile Pro Ile Ile Leu Phe Gly Ser Ser Asn
 355 360 365
 Ala Met Ser Phe Ala Pro Asn Ser Val Ile Ala Leu Arg Asp Val Pro
 370 375 380
 Gln Asp Leu Val Gly Ser Ala Ser Gly Phe Tyr Asn Thr Ser Arg Gln

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Val Gly Ala Val Leu Gly Ala Ala Thr Leu Gly Ala Val Met Gln Ile
                      405                      410                      415

Gly Val Gly Thr Val Ser Phe Gly Val Ala Met Gly Ala Ala Ile Leu
                      420                      425                      430

Val Thr Leu Val Pro Leu Ile Phe Gly Phe Leu Ala Val Thr Gln Phe
                      435                      440                      445

Arg

<210> 261
<211> 1338
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1315)
<223> RXA02088

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                      Met Leu Thr Gln Lys
                      1                      5

ata gaa tta gag gct aaa cca aaa atc cca gag gag atc tgg gtg ctg 163
Ile Glu Leu Glu Ala Lys Pro Lys Ile Pro Glu Glu Ile Trp Val Leu
                      10                      15                      20

gtt gtg gct gcg ttt att att gcg ctg ggc tat ggc ctg att gcg ccg 211
Val Val Ala Ala Phe Ile Ile Ala Leu Gly Tyr Gly Leu Ile Ala Pro
                      25                      30                      35

att ttg cca cag ttt gtg gtc ggt ttt gat gta agt ttt gca gct gcc 259
Ile Leu Pro Gln Phe Val Val Gly Phe Asp Val Ser Phe Ala Ala Ala
                      40                      45                      50

agt gcg gtg gtg tcc atc ttt gcg ggc gcc cgg ttg ttg ttt gcg ccg 307
Ser Ala Val Val Ser Ile Phe Ala Gly Ala Arg Leu Leu Phe Ala Pro
                      55                      60                      65

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Met Ser Gly Ser Leu Ile Asp Lys Ile Gly Ser Arg Arg Val Tyr Leu
                      70                      75                      80                      85

act ggt tta ctc acc gtg gct atc acc acg ggg ctt gtt gcg ttg gcg 403
Thr Gly Leu Leu Thr Val Ala Ile Thr Thr Gly Leu Val Ala Leu Ala
                      90                      95                      100

cag gaa tac tgg cag att ctg ctg ctt cgt ggc atc gca ggt att ggt 451
Gln Glu Tyr Trp Gln Ile Leu Leu Leu Arg Gly Ile Ala Gly Ile Gly
                      105                      110                      115

tcc acc atg ttt acg gtc tct gcc atg ggc ctg atc gtg aag atg gcg 499

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Pro Val Glu Ile Arg Gly Arg Cys Ser Ser Val Tyr Ala Ser Ser Phe	
135 140 145	
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Leu Phe Gly Asn Ile Ile Gly Pro Val Val Gly Ala Ala Met Ser Gly	
150 155 160 165	
ttg ggc atg cgc tgg cgc ttc cgc att tat ggt gct tcc gtt ggc tta	643
Leu Gly Met Arg Trp Pro Phe Ala Ile Tyr Gly Ala Ser Val Gly Leu	
170 175 180	
gct gca ctt gtt gtg tgg tgg cgc atg cgc aaa acc aac gat tca ctt	691
Ala Ala Leu Val Val Trp Trp Arg Met Pro Lys Thr Asn Asp Ser Leu	
185 190 195	
cgg aag gct gat agc aat agt gtg cgc gcg ttg cgc ttt gct gag gca	739
Arg Lys Ala Asp Ser Asn Ser Val Pro Ala Leu Arg Phe Ala Glu Ala	
200 205 210	
att aag gat tct gcc tac cgc tgc gcg ttg ttt agt gct ttt gcc aat	787
Ile Lys Asp Ser Ala Tyr Arg Ser Ala Leu Phe Ser Ala Phe Ala Asn	
215 220 225	
ggt tgg tgc aac ttt ggt gtg cgt gtg gcg gtt ctt cca ctg ttt gcc	835
Gly Trp Ser Asn Phe Gly Val Arg Val Ala Val Leu Pro Leu Phe Ala	
230 235 240 245	
gca gct gca ttt agc aat ggc gga gct att gcg ggt ttt gcc atg gct	883
Ala Ala Ala Phe Ser Asn Gly Gly Ala Ile Ala Gly Phe Ala Met Ala	
250 255 260	
gcg ttc gcc gct gga aat gct ttg tgt ctg caa ttc gcg gcc gat ctg	931
Ala Phe Ala Ala Gly Asn Ala Leu Cys Leu Gln Phe Ala Asp Leu	
265 270 275	
tca gat cgc att ggc cgt aaa cgc atg att att tcc ggg ctg atc gtc	979
Ser Asp Arg Ile Gly Arg Lys Pro Met Ile Ile Ser Gly Leu Ile Val	
280 285 290	
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Asn Ala Val Phe Thr Ala Met Ile Gly Phe Gly Thr Glu Val Trp Ile	
295 300 305	
ctg atc acg gta tct gcg ttg gca ggt gct ggt gcg ggc ttg ctt aat	1075
Leu Ile Thr Val Ser Ala Leu Ala Gly Ala Gly Ala Gly Leu Leu Asn	
310 315 320 325	
cca agt cag cag gcg gtg ctc gct gat gtt ata gat tcc cgc ccc ggc	1123
Pro Ser Gln Gln Ala Val Leu Ala Asp Val Ile Asp Ser Arg Pro Gly	
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Gly Lys Val Leu Ala Asn Phe Gln Met Ala Gln Asp Phe Gly Ala Ile	
345 350 355	
gtt ggc cgc att ctg gta ggc atg atc gca gaa cag gca gcc ttc caa	1219
Val Gly Pro Ile Leu Val Gly Met Ile Ala Glu Gln Ala Gly Phe Gln	

00603200 062300 502250

Ser Ala Phe Ala Asn Gly Trp Ser Asn Phe Gly Val Arg Val Ala Val
 225 230 235 240
 Leu Pro Leu Phe Ala Ala Ala Ala Phe Ser Asn Gly Gly Ala Ile Ala
 245 250 255
 Gly Phe Ala Met Ala Ala Phe Ala Ala Gly Asn Ala Leu Cys Leu Gln
 260 265 270
 Phe Ala Gly Asp Leu Ser Asp Arg Ile Gly Arg Lys Pro Met Ile Ile
 275 280 285
 Ser Gly Leu Ile Val Asn Ala Val Phe Thr Ala Met Ile Gly Phe Gly
 290 295 300
 Thr Glu Val Trp Ile Leu Ile Thr Val Ser Ala Leu Ala Gly Ala Gly
 305 310 315 320
 Ala Gly Leu Leu Asn Pro Ser Gln Gln Ala Val Leu Ala Asp Val Ile
 325 330 335
 Asp Ser Arg Pro Gly Gly Lys Val Leu Ala Asn Phe Gln Met Ala Gln
 340 345 350
 Asp Phe Gly Ala Ile Val Gly Pro Ile Leu Val Gly Met Ile Ala Glu
 355 360 365
 Gln Ala Gly Phe Gln Ile Gly Phe Met Leu Cys Gly Val Ile Ser Leu
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 385 390 395 400
 Lys Val Glu Gln Val
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 <223> RXA00764

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 Met Thr Leu Lys Thr
 1 5
 agc gtt ttg gca cta ctc tta gat aac gtg cat gtt ctt ctg att gcg 163
 Ser Val Leu Ala Leu Leu Leu Asp Asn Val His Val Leu Leu Ile Ala
 10 15 20
 aat cct gag tgg acc acg cag acg cag aaa ctt ttc cgt cgt gtg gtg 211
 Asn Pro Glu Ser Thr Thr Gln Thr Gln Lys Leu Phe Arg Arg Val Val
 25 30 35

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cac ctg att ggc gtg ggg cat ggt cgg aag ttg gag aag ttg atc gct 979
 His Leu Ile Gly Val Gly His Gly Arg Lys Leu Glu Lys Leu Ile Ala
 280 285 290

aag cgc acc att gct ttt gat gat gcg gag aaa gta acg ctc acg tgc 1027
 Lys Arg Thr Ile Ala Phe Asp Asp Ala Glu Lys Val Thr Leu Thr Cys
 295 300 305

gac agc gat cag cgt ttc caa gtt gat ggt gag tat gaa ggc aaa cca 1075
 Asp Ser Asp Gln Arg Phe Gln Val Asp Gly Glu Tyr Glu Gly Lys Pro
 310 315 320 325

aca aag gtg gtg ttg gaa tca atc act gat gcg gtg cga gtg tat gcg 1123
 Thr Lys Val Val Leu Glu Ser Ile Thr Asp Ala Val Arg Val Tyr Ala
 330 335 340

ccg aag acg cat ccg aca ccg ccg atc atg aat tgg gct gtc cat ttg 1171
 Pro Lys Thr His Pro Thr Pro Ile Met Asn Trp Ala Val His Leu
 345 350 355

ttt aag cac gtc cgt gat ttc ctc cgg gtg cgc acg ttt ggc atc 1216
 Phe Lys His Val Arg Asp Phe Leu Arg Val Arg Thr Phe Gly Ile
 360 365 370

taggattcat cggagttttc ttc 1239

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 <211> 372
 <212> PRT
 <213> Corynebacterium glutamicum

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Val Leu Leu Ile Ala Asn Pro Glu Ser Thr Thr Gln Thr Gln Lys Leu
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Phe Arg Arg Val Val Pro Ala Leu Met Ala Leu Asp Gly Val Ser Leu
 35 40 45

Glu Ala Arg Phe Thr His Tyr Gly Gly His Ala Glu Glu Met Val Ala
 50 55 60

Gly Leu Thr Val Asp Asp Phe Asp Val Ile Ile Pro Ala Gly Gly Asp
 65 70 75 80

Gly Thr Val Asn Glu Val Ile Asn Gly Leu Leu Gly Ser Ala Glu Gly
 85 90 95

Asp Phe Arg Asn Leu Glu Asp Leu Pro Ala Ile Ala Val Leu Pro Thr
 100 105 110

Gly Ser Ala Asn Val Phe Ala Arg Ala Leu Gly Tyr Pro Thr Asp Pro
 115 120 125

Tyr Ala Ala Ala Asp Ala Leu Val Glu Leu Ile Arg Lys Asn His Thr
 130 135 140

Arg Thr Ile Thr Leu Gly Thr Trp Lys Gly Asp Asp Gln Gly Thr Arg

002290-00230961

145					150										155														160
Trp	Phe	Ala	Val	Asn	Ala	Gly	Phe	Gly	Ile	Asp	Ala	Asp	Val	Ile	Ala														
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Arg	Val	Glu	Arg	Ala	Arg	Ser	Phe	Gly	Phe	Ala	Ala	Ser	Pro	Leu	Leu														
			180					185					190																
Tyr	Leu	Gln	Val	Ser	Leu	Arg	Ala	Trp	Val	Lys	Thr	Gln	Ile	Lys	Pro														
		195					200					205																	
Pro	Lys	Ile	Thr	Val	Glu	Ala	Val	Asp	Ser	Lys	Gly	His	Lys	Leu	Gln														
		210				215					220																		
Lys	Glu	Glu	Val	Pro	Met	Leu	Leu	Ala	Ser	Asn	Thr	Asn	Pro	Trp	Thr														
		225			230					235																			
Phe	Leu	Gly	Pro	Leu	Pro	Val	Val	Thr	Asn	Pro	Gln	Asn	Ser	Phe	Asp														
				245					250					255															
Thr	Gly	Leu	Gly	Leu	Phe	Gly	Leu	Thr	Ser	Val	Arg	Gly	Phe	Gly	Gly														
			260					265					270																
Val	Ala	Ala	Met	Met	His	Leu	Ile	Gly	Val	Gly	His	Gly	Arg	Lys	Leu														
		275					280					285																	
Glu	Lys	Leu	Ile	Ala	Lys	Arg	Thr	Ile	Ala	Phe	Asp	Asp	Ala	Glu	Lys														
		290				295					300																		
Val	Thr	Leu	Thr	Cys	Asp	Ser	Asp	Gln	Arg	Phe	Gln	Val	Asp	Gly	Glu														
		305			310					315																			
Tyr	Glu	Gly	Lys	Pro	Thr	Lys	Val	Val	Leu	Glu	Ser	Ile	Thr	Asp	Ala														
				325					330					335															
Val	Arg	Val	Tyr	Ala	Pro	Lys	Thr	His	Pro	Thr	Pro	Pro	Ile	Met	Asn														
			340					345					350																
Trp	Ala	Val	His	Leu	Phe	Lys	His	Val	Arg	Asp	Phe	Leu	Arg	Val	Arg														
		355					360						365																
Thr	Phe	Gly	Ile					</																					

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163
Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
10 15 20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
25 30 35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259
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<210> 266

<211> 57

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 266

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Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
35 40 45

Asp Asp Pro Gln Pro Leu Leu Cys Phe
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<210> 267

<211> 1443

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

 $\langle 222 \rangle$ (101) .. (1420)

<223> RXN01553

<400> 267

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taccaagcca gacttaaatt tctaccttaa agtctttgagc atg act gtt cag gaa 115
Met Thr Val Gln Glu
1 5

ttc gac cgc gcg acc aaa ccc aca cca aaa ccc cca att gtt tct tgg 163
Phe Asp Arg Ala Thr Lys Pro Thr Pro Lys Pro Pro Ile Val Ser Trp
10 15 20

gcg ttt tgg gat tgg ggt tcc gcc tct ttc aac gcg gtc ctc gtg acc 211
Ala Phe Trp Asp Trp Gly Ser Ala Ser Phe Asn Ala Val Leu Val Thr
25 30 35

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Gly Arg Arg Ser Asp Ile Lys Gly Thr Arg Arg Arg Ser Leu Arg Met		
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Trp Thr Leu Val Thr Val Phe Leu Met Phe Cys Leu Phe Thr Val Lys		
	100	105
Asn Thr Asp Pro Thr Phe Phe Trp Phe Gly Val Ala Ile Met Ala Ile		
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Ala Asn Ile Thr Phe Glu Phe Ala Glu Val Gln Tyr Tyr Ala Gln Leu		
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Ser Gln Ile Ser Thr Arg Glu Asn Val Gly Arg Val Ser Gly Phe Gly		
	145	150
Trp Ser Met Gly Tyr Phe Gly Gly Ile Val Leu Leu Leu Val Cys Tyr		
	165	170
Leu Gly Phe Val Ala Gly Asp Gly Asp Thr Arg Gly Phe Leu Asn Leu		
	180	185
Pro Ile Glu Asp Gly Met Asn Ile Arg Leu Val Ala Val Leu Ala Ala		
	195	200
Val Trp Phe Leu Val Ser Ala Ile Pro Ala Leu Leu Arg Val Pro Glu		
	210	215
Ile Glu Ala Gln Val Ala Ala Glu Asp His Pro Lys Gly Leu Ile Ala		
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Ala Tyr Lys Asp Leu Phe Gly Gln Ile Ala Glu Leu Trp Lys Gln Asp		
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Arg Asn Ser Val Tyr Phe Leu Ile Ala Ala Thr Val Phe Arg Asp Gly		
	260	265
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Gly Leu Ser Ala Gly Asp Val Leu Leu Phe Gly Val Ala Ala Asn Val		
	290	295
Val Ser Ala Leu Gly Ala Leu Leu Gly Gly Phe Leu Asp Asp Arg Val		
	305	310
Gly Pro Lys Pro Ile Ile Leu Ile Ser Leu Ala Ile Met Ile Ala Asp		
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Ala Ala Ile Leu Phe Phe Val Glu Gly Pro Thr Asn Phe Trp Ile Phe		
	340	345
Gly Leu Ile Leu Cys Ala Phe Val Gly Pro Ala Gln Ser Ala Ser Arg		
	355	360
Ser Tyr Leu Thr Arg Leu Ser Pro Asp Gly Gln Glu Gly Gln Leu Phe		
	370	375

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Gly Leu Tyr Ala Thr Thr Gly Arg Ala Val Ser Trp Met Val Pro Ser
385 390 395 400

Leu Phe Gly Val Phe Val Gly Leu Thr Gly Asp Asp Arg Thr Gly Ile
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Leu Ala Ile Ala Leu Ile Leu Leu Phe Gly Ile Val Leu Leu Ser Met
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Val Lys Pro Pro His Lys Val Lys
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<210> 269

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<212> DNA

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<223> RXN00535

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cctaaggagc tcacctttac tcaatgctct gatgacaccg atg tgg tgg gca ggc 115
Met Trp Trp Ala Gly
1 5

atg agt acc gcg atg ctg gca tat ttc tta caa aca gta gca ctt ggt 163
Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln Thr Val Ala Leu Gly
10 15 20

ttc ggc acc ctc ttg gta gtg caa cca gtg ctt gtc ctg tgc ctg atg 211
Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu Val Leu Ser Leu Met
25 30 35

ttc acg ctg ccg ctc tca gca cga ttc aat ggc tac cga cta cgc cga 259
Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly Tyr Arg Leu Arg Arg
40 45 50

act gaa atc ttc tgg gct acc ctc ctc acc gta gcc gtg ggc atc atg 307
Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val Ala Val Gly Ile Met
55 60 65

atc gtt ttg gga cgc ccc ctt ccc gga aac ccc cac ccc cca ctc gat 355
Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro His Pro Pro Leu Asp
70 75 80 85

cga tgg att cca gta ctt tta gtc ggc gtt gca gta atg ggt gga atg 403
Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala Val Met Gly Gly Met
90 95 100

tggt ctg ctt gcg gaa tac gta tta aag aag gac aaa gcc ctc atc ctt 451
Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp Lys Ala Leu Ile Leu
105 110 115

ggt ctt gtg acg ggt gca ttg ttt ggc tac gta gca gtg atg tcc aaa 499
Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val Ala Val Met Ser Lys

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120	125	130	
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Ala Ala Val Asp Leu Phe Val His Gln Gly Ile Thr Gly Leu Ile Leu			
135	140	145	
aac tgg gaa ggc tac ggc cta atc ctc acc gca tta ctt gga aca atc			595
Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala Leu Leu Gly Thr Ile			
150	155	160	165
gtg cag cag tat tcc ttt aac gct ggc gaa cta caa aaa tcg cta ccc			643
Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu Gln Lys Ser Leu Pro			
170	175	180	
gcc atg acc att gcc gaa cca att gtt gcc ttc agt ttg ggc tac ttg			691
Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe Ser Leu Gly Tyr Leu			
185	190	195	
gtt ctg ggc gaa aaa ttc caa gtc gtg gac tgg gaa tgg atc gcc atg			739
Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp Glu Trp Ile Ala Met			
200	205	210	
ggc atc gca cta ctg gtg atg att gtt tcc acc att gca ctg tct cgt			787
Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr Ile Ala Leu Ser Arg			
215	220	225	
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Thr Ser Thr Met Pro Ala Gly Ser Lys Arg			
230	235		
cga			840
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Thr Val Ala Leu Gly Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu			
20	25	30	
Val Leu Ser Leu Met Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly			
35	40	45	
Tyr Arg Leu Arg Arg Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val			
50	55	60	
Ala Val Gly Ile Met Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro			
65	70	75	80
His Pro Pro Leu Asp Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala			
85	90	95	
Val Met Gly Gly Met Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp			
100	105	110	
Lys Ala Leu Ile Leu Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val			

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115 120 125

Ala Val Met Ser Lys Ala Ala Val Asp Leu Phe Val His Gln Gly Ile
130 135 140

Thr Gly Leu Ile Leu Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala
145 150 155 160

Leu Leu Gly Thr Ile Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu
165 170 175

Gln Lys Ser Leu Pro Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe
180 185 190

Ser Leu Gly Tyr Leu Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp
195 200 205

Glu Trp Ile Ala Met Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr
210 215 220

Ile Ala Leu Ser Arg Thr Ser Thr Met Pro Ala Gly Ser Lys Arg
225 230 235

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<211> 2472
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(2449)
<223> RXN00453

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Val Ile Ser Ala Trp
1 5

cta ctt att ttg gcc att gtt ggt ggt ctg gcc ctg acg atg cag aag 163
Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala Leu Thr Met Gln Lys
10 15 20

ggg ttc agt aac tct ttc act att gaa gac acc cct tcg att gat gcc 211
Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr Pro Ser Ile Asp Ala
25 30 35

act gtt tct ctg gtt gaa aat ttc cct gat cag acg aac ccg gtg acg 259
Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln Thr Asn Pro Val Thr
40 45 50

gcc gcc gga gtt aac gtg gtt ttc caa tcc ccg gaa gga acc acg ctt 307
Ala Ala Gly Val Asn Val Phe Gln Ser Pro Glu Gly Thr Thr Leu
55 60 65

gat gat cct cag atg atg act gcg atg gat gca gtc gtt gat tac att 355
Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala Val Val Asp Tyr Ile
70 75 80 85

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09802620

Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala Leu Thr Phe Ile Pro	330	335	340	
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Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe Lys Gly Lys Ile Pro	345	350	355	
gga att ggt gga aac cca acg cca aag cag acg tgg gag caa gcg ctt				1219
Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr Trp Glu Gln Ala Leu	360	365	370	
aat cgt cgt tcc aag ggt cgc tca tgg gtc aag ctt gta cag aaa gca				1267
Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys Leu Val Gln Lys Ala	375	380	385	
ccg ggt ctt gtg gtg gca gtg gtg gtc ttg ggt ctt ggt gcc ttg acc				1315
Pro Gly Leu Val Val Ala Val Val Val Leu Gly Leu Gly Ala Leu Thr	390	395	400	405
att cct gca atg aac ctg cag ttg tca ctg cct tct gac tcc acc tcc				1363
Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro Ser Asp Ser Thr Ser	410	415	420	
aat att gat acc act cag cgt cag tcg gct gat ttg atg gca gag ggc				1411
Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp Leu Met Ala Glu Gly	425	430	435	
ttt ggc gcg ggc gtt aat gcg ccg ttc ttg gtc atc gtc gat acg cat				1459
Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val Ile Val Asp Thr His	440	445	450	
gag gtc aat gct gat tcc acc gca ttg cag cca ctg att gag gca cag				1507
Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro Leu Ile Glu Ala Gln	455	460	465	
gag cct gaa gag ggc gag ttc gat ccg gag cag gcg gct cgt ttt gct				1555
Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln Ala Ala Arg Phe Ala	470	475	480	485
acc tat atg tat gtc acc cag acc tac aat tcc aac atc gat gtg aag				1603
Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser Asn Ile Asp Val Lys	490	495	500	
aat gcg cag atc atc agc gtc aat gat gat ttc act gcg gcg cag att				1651
Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe Thr Ala Ala Gln Ile	505	510	515	
ctc gtg act cca tac acc gga cct gcg gat aaa gag acc cct gag ttg				1699
Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys Glu Thr Pro Glu Leu	520	525	530	
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Met His Val Leu Arg Ala Gln Glu Ala Gln Ile Glu Asp Val Thr Gly	535	540	545	
act gaa ctg ggt acc act ggg ttt acg gcg gtt cag ttg gac att act				1795
Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val Gln Leu Asp Ile Thr	550	555	560	565
gag cag ctg gaa gac gca atg ccg gtt tac ctc gct gtg gtt gtt ggt				1843
Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu Ala Val Val Val Gly				

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570	575	580	
ttg gct att ttc ctc ctc att ctg gtg ttc cgt tcc ctg ctt gtt ccg Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg Ser Leu Leu Val Pro	585	590	595 1891
ctg gtt gct ggc ctt ggc ttc ttg ttg tct gtg ggt gcg gcc ttc ggt Leu Val Ala Gly Leu Gly Phe Leu Ser Val Gly Ala Ala Phe Gly	600	605	610 1939
gcg acg gtg ttg gtc tgg cag gag ggc ttc ggt ggc ttt gtg aac acc Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly Gly Phe Val Asn Thr	615	620	625 1987
cct ggt ccg ctg att tcc ttc atg ccg atc ttc ctc atc gcc gtg acc Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe Leu Ile Gly Val Thr	630	635	640 645 2035
ttc ggt ttg gcc atg gac tat cag gtg ttc ctt gtg act cgc atg cgc Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu Val Thr Arg Met Arg	650	655	660 2083
gag cac tac acc cac cac aat gcc aag gga cag cct ggt tcc aag tac Glu His Tyr Thr His His Asn Gly Lys Gly Gln Pro Gly Ser Lys Tyr	665	670	675 2131
acc ccg gtt gag cag tca gtg att gaa gcc ttc acg cag gcc tcc cgc Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe Thr Gln Gly Ser Arg	680	685	690 2179
gtg gtt aca gca gcg gca ctg atc atg att gcc gtg ttc gtg gcg ttt Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala Val Phe Val Ala Phe	695	700	705 2227
att gat cag ccg ttg cca ttt att aag atc ttc ggt ttc gcg ttg ggt Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe Gly Phe Ala Leu Gly	710	715	720 725 2275
gcg gcc gtg ttt ttc gat gct ttc ttc att cgc atg ggt ctg gtc ccc Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg Met Gly Leu Val Pro	730	735	740 2323
gcg tcg atg ttc ctg atg gcc aag gcc acg tgg tgg atg cct aag tgg Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp Trp Met Pro Lys Trp	745	750	755 2371
ctg gat cga att ctg cca agt ttg gac att gaa gcc acc gca ctg gag Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu Gly Thr Ala Leu Glu	760	765	770 2419
aag gaa tgg gag gag aag cag gct gca cgt tagacttgcc acctatgtca Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg	775	780	2469
gat			2472

<210> 272

<211> 783

<212> PRT

<213> Corynebacterium glutamicum

00603208-062300

Val	Ile	Ser	Ala	Trp	Leu	Leu	Ile	Leu	Ala	Ile	Val	Gly	Gly	Leu	Ala
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Leu	Thr	Met	Gln	Lys	Gly	Phe	Ser	Asn	Ser	Phe	Thr	Ile	Glu	Asp	Thr
			20					25					30		
Pro	Ser	Ile	Asp	Ala	Thr	Val	Ser	Leu	Val	Glu	Asn	Phe	Pro	Asp	Gln
		35					40					45			
Thr	Asn	Pro	Val	Thr	Ala	Ala	Gly	Val	Asn	Val	Val	Phe	Gln	Ser	Pro
50					55						60				
Glu	Gly	Thr	Thr	Leu	Asp	Asp	Pro	Gln	Met	Met	Thr	Ala	Met	Asp	Ala
65				70						75				80	
Val	Val	Asp	Tyr	Ile	Glu	Asp	Asn	Leu	Pro	Asp	Phe	Gly	Gly	Gly	Glu
				85				90						95	
Arg	Phe	Gly	Asn	Pro	Val	Glu	Val	Ser	Pro	Ala	Leu	Glu	Glu	Met	Val
		100						105					110		
Ile	Glu	Gln	Met	Thr	Ser	Met	Gly	Leu	Pro	Glu	Glu	Thr	Ala	Ala	Lys
		115					120					125			
Asp	Ala	Ala	Asn	Leu	Ala	Val	Leu	Ser	Glu	Asp	Lys	Thr	Ile	Gly	Tyr
130						135				140					
Thr	Ser	Phe	Asn	Ile	Asp	Val	Glu	Ala	Ala	Glu	Tyr	Val	Glu	Gln	Lys
145				150						155				160	
His	Arg	Asp	Val	Ile	Asn	Glu	Ala	Met	Gln	Ile	Gly	Glu	Asp	Leu	Gly
			165					170						175	
Val	Arg	Val	Glu	Ala	Gly	Gly	Pro	Ala	Phe	Gly	Asp	Pro	Ile	Gln	Ile
		180					185						190		
Glu	Thr	Thr	Ser	Glu	Ile	Ile	Gly	Ile	Gly	Ile	Ala	Phe	Ile	Val	Leu
		195					200				205				
Ile	Phe	Thr	Phe	Gly	Ser	Leu	Ile	Ala	Ala	Gly	Leu	Pro	Leu	Ile	Thr
210						215				220					
Ala	Val	Ile	Gly	Val	Gly	Ile	Gly	Ala	Leu	Ala	Ile	Val	Leu	Ala	Thr
225				230					235					240	
Ala	Phe	Thr	Asp	Leu	Asn	Asn	Val	Thr	Pro	Val	Leu	Ala	Val	Met	Ile
			245					250						255	
Gly	Leu	Ala	Val	Gly	Ile	Asp	Tyr	Ala	Leu	Phe	Ile	Leu	Ser	Arg	Tyr
		260						265					270		
Arg	Ala	Glu	Tyr	Lys	Arg	Met	Pro	Arg	Ala	Asp	Ala	Ala	Gly	Met	Ala
275						280					285				
Val	Gly	Thr	Ala	Gly	Ser	Ala	Val	Val	Phe	Ala	Gly	Ala	Thr	Val	Ile
					295					300					
Ile	Ala	Leu	Val	Ala	Leu	Ile	Ile	Ala	Asp	Ile	Gly	Phe	Leu	Thr	Ala
305				310					315					320	

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Met Gly Ile Ser Ala Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala
 325 330 335
 Leu Thr Phe Ile Pro Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe
 340 345 350
 Lys Gly Lys Ile Pro Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr
 355 360 365
 Trp Glu Gln Ala Leu Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys
 370 375 380
 Leu Val Gln Lys Ala Pro Gly Leu Val Val Ala Val Val Val Leu Gly
 385 390 395 400
 Leu Gly Ala Leu Thr Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro
 405 410 415
 Ser Asp Ser Thr Ser Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp
 420 425 430
 Leu Met Ala Glu Gly Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val
 435 440 445
 Ile Val Asp Thr His Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro
 450 455 460
 Leu Ile Glu Ala Gln Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln
 465 470 475 480
 Ala Ala Arg Phe Ala Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser
 485 490 495
 Asn Ile Asp Val Lys Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe
 500 505 510
 Thr Ala Ala Gln Ile Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys
 515 520 525
 Glu Thr Pro Glu Leu Met His Val Leu Arg Ala Gln Glu Ala Gln Ile
 530 535 540
 Glu Asp Val Thr Gly Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val
 545 550 555 560
 Gln Leu Asp Ile Thr Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu
 565 570 575
 Ala Val Val Val Gly Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg
 580 585 590
 Ser Leu Leu Val Pro Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val
 595 600 605
 Gly Ala Ala Phe Gly Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly
 610 615 620
 Gly Phe Val Asn Thr Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe
 625 630 635 640

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Leu Ile Gly Val Thr Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu
 645 650 655
 Val Thr Arg Met Arg Glu His Tyr Thr His His Asn Gly Lys Gly Gln
 660 665 670
 Pro Gly Ser Lys Tyr Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe
 675 680 685
 Thr Gln Gly Ser Arg Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala
 690 695 700
 Val Phe Val Ala Phe Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe
 705 710 715 720
 Gly Phe Ala Leu Gly Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg
 725 730 735
 Met Gly Leu Val Pro Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp
 740 745 750
 Trp Met Pro Lys Trp Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu
 755 760 765
 Gly Thr Ala Leu Glu Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg
 770 775 780

<210> 273
 <211> 597
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(574)
 <223> RXN00932

<400> 273
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 aataaggtga tgtttcaacg attaggttac ggtaggggcc atg acg cca cag aaa 115
 Met Thr Pro Gln Lys
 1 5
 ctt cac cgt ttt gca gcc ctt tta gaa atg ggt acc tgg acc ctg ctg 163
 Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly Thr Trp Thr Leu Leu
 10 15 20
 atc atc ggc atg atc tta aaa tac agt gga gtg aca gac gcc gta acc 211
 Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val Thr Asp Ala Val Thr
 25 30 35
 cct att gcc ggc ggt atc cac ggc ttt ggc ttc ctg tgt ttt gca gcc 259
 Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe Leu Cys Phe Ala Ala
 40 45 50
 atc acc atc acc gtg tgg atc aat aat aag tgg aca ttc ccg cag ggt 307
 Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp Thr Phe Pro Gln Gly
 55 60 65

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[illegible]

145

150

155

<210> 275
 <211> 534
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <222> (65)..(511)
 <223> RXN03022

<400> 275
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 agcagtg atc atc acc gct ggc atc ttg gta gcg acc gcg acc gcc ctc 109
 Val Ile Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu
 1 5 10 15
 cta atg atc acc gcg gtc agc gag tca acg tac atc gtc atc tcc ctc 157
 Leu Met Ile Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu
 20 25 30
 gcc gcc ttc tcc ctt tat ggc ctt ggc ctc gga ctc ttc gcc acc cca 205
 Ala Gly Phe Ser Leu Tyr Gly Leu Gly Leu Phe Ala Thr Pro
 35 40 45
 gtc acc gat act gcg ctt gga aca ctt ccc aaa gac cgt acc ggc gct 253
 Val Thr Asp Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala
 50 55 60
 ggt gca ggt gta ttc aag atg tcc tct tcc ctc ggc gca gca ctc ggc 301
 Gly Ala Gly Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly
 65 70 75
 atc gca atc tcc act tca gtg ttc ctc gca ctt cgc gac gcc acc tcc 349
 Ile Ala Ile Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser
 80 85 90 95
 atc aac tcc gac gtc gca ctc gcc gga aca gtt tca ctt gcc atc aac 397
 Ile Asn Ser Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn
 100 105 110
 gtt gta ttc gca gca aca gcc acc atc acc gca gca gtc ctt att cca 445
 Val Val Phe Ala Ala Thr Ala Thr Ile Thr Ala Ala Val Leu Ile Pro
 115 120 125
 aaa gcc gct ggc aaa gtc tca caa acc agc atc acc ctt cct gag cca 493
 Lys Ala Ala Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro
 130 135 140
 gct atc gct gta aaa atc taaaacttca ccaggacaga taa 534
 Ala Ile Ala Val Lys Ile
 145

<210> 276
 <211> 149
 <212> PRT
 <213> *Corynebacterium glutamicum*

002290-802E0960

<400> 276

Val Ile Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu Leu
 1 5 10 15

Met Ile Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu Ala
 20 25 30

Gly Phe Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro Val
 35 40 45

Thr Asp Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala Gly
 50 55 60

Ala Gly Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly Ile
 65 70 75 80

Ala Ile Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser Ile
 85 90 95

Asn Ser Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn Val
 100 105 110

Val Phe Ala Ala Thr Ala Thr Ile Thr Ala Ala Val Leu Ile Pro Lys
 115 120 125

Ala Ala Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro Ala
 130 135 140

Ile Ala Val Lys Ile
 145

<210> 277

<211> 586

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(586)

<223> RXN03151

<400> 277

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agtatttgtt taaccatcca cctcaaggag taaaacgcac gtg ctt tcc cac atc 115
 Val Leu Ser His Ile
 1 5

att gat gtc ctc gcc gac ccg atc gat ggc acc cca ctt gta ggc gcc 163
 Ile Asp Val Leu Ala Asp Pro Ile Asp Gly Thr Pro Leu Val Gly Ala
 10 15 20

gaa gat ttc tca cgg ttg gtg tct gaa tct ggg cat tcc tac gat gtt 211
 Glu Asp Phe Ser Arg Leu Val Ser Glu Ser Gly His Ser Tyr Asp Val
 25 30 35

gct cgt caa ggg tat gtc acc ctg gct ggt ggc gca ggt ctg cgc tat 259
 Ala Arg Gln Gly Tyr Val Thr Leu Ala Gly Gly Ala Gly Leu Arg Tyr
 40 45 50

006290-80250560

tca ggc gat gat gca cag atg atc gcg gat cgg gaa acc ttc ctt tct 307
 Ser Gly Asp Asp Ala Gln Met Ile Ala Asp Arg Glu Thr Phe Leu Ser
 55 60 65

ggc ggt cac ttc gcg ccc ttc gtg gaa gct gtc acc gag cat gtt caa 355
 Gly Gly His Phe Ala Pro Phe Val Glu Ala Val Thr Glu His Val Gln
 70 75 80 85

gat gtc gtt gac cag gca ggc ctt agc gat gac gca cag cca gtg gtc 403
 Asp Val Val Asp Gln Ala Gly Leu Ser Asp Asp Ala Gln Pro Val Val
 90 95 100

tgc gaa atc ggc gcg gga acc ggc tac tac ttg tcc cat acc ctt gat 451
 Cys Glu Ile Gly Ala Gly Thr Gly Tyr Tyr Leu Ser His Thr Leu Asp
 105 110 115

tct gtt gca gga tct cgc gga att ggc att gac gtt tcc gtg cac gcc 499
 Ser Val Ala Gly Ser Arg Gly Ile Gly Ile Asp Val Ser Val His Ala
 120 125 130

gca aag cgt ttg gca aag tgt cac cct cgc gtc ggc gca gtc atc gcg 547
 Ala Lys Arg Leu Ala Lys Cys His Pro Arg Val Gly Ala Val Ile Ala
 135 140 145

aac gca tgg gca cgc ctg ccg att gca gat aac tcc tcg 586
 Asn Ala Trp Ala Arg Leu Pro Ile Ala Asp Asn Ser Ser
 150 155 160

<210> 278
 <211> 162
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 278
 Val Leu Ser His Ile Ile Asp Val Leu Ala Asp Pro Ile Asp Gly Thr
 1 5 10 15

Pro Leu Val Gly Ala Glu Asp Phe Ser Arg Leu Val Ser Glu Ser Gly
 20 25 30

His Ser Tyr Asp Val Ala Arg Gln Gly Tyr Val Thr Leu Ala Gly Gly
 35 40 45

Ala Gly Leu Arg Tyr Ser Gly Asp Asp Ala Gln Met Ile Ala Asp Arg
 50 55 60

Glu Thr Phe Leu Ser Gly Gly His Phe Ala Pro Phe Val Glu Ala Val
 65 70 75 80

Thr Glu His Val Gln Asp Val Val Asp Gln Ala Gly Leu Ser Asp Asp
 85 90 95

Ala Gln Pro Val Val Cys Glu Ile Gly Ala Gly Thr Gly Tyr Tyr Leu
 100 105 110

Ser His Thr Leu Asp Ser Val Ala Gly Ser Arg Gly Ile Gly Ile Asp
 115 120 125

Val Ser Val His Ala Ala Lys Arg Leu Ala Lys Cys His Pro Arg Val

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130 135 140

Gly Ala Val Ile Ala Asn Ala Trp Ala Arg Leu Pro Ile Ala Asp Asn
 145 150 155 160

Ser Ser

<210> 279
 <211> 543
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(543)
 <223> RXN02832

<400> 279
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 Arg Gly Pro Val Met Asp Tyr Thr Asn Gln Ser Leu Val Ala Phe Phe
 1 5 10 15

ttt aaa gca tta acg tca tat tta aag aaa cac aat tgt tta tat gtc 96
 Phe Lys Ala Leu Thr Ser Tyr Leu Lys Lys His Asn Cys Leu Tyr Val
 20 25 30

ctt gta gat cca tat tta att gaa aat tta cgc aat gca gac ggt gaa 144
 Leu Val Asp Pro Tyr Leu Ile Glu Asn Leu Arg Asn Ala Asp Gly Glu
 35 40 45

att gtt aaa tct tat gat aac cga gca ttt gtt aga aca atg gat aaa 192
 Ile Val Lys Ser Tyr Asp Asn Arg Ala Phe Val Arg Thr Met Asp Lys
 50 55 60

tta ggt tat aaa cac caa ggt ttc cct gta ggt tat gat tca atg agc 240
 Leu Gly Tyr Lys His Gln Gly Phe Pro Val Gly Tyr Asp Ser Met Ser
 65 70 75 80

caa atc cgt tgg ctg tca gtg tta gat tta aaa gat aag act gaa gac 288
 Gln Ile Arg Trp Leu Ser Val Leu Asp Leu Lys Asp Lys Thr Glu Asp
 85 90 95

caa ctt tta aaa gaa atg gat tat caa acg aga cgt aat att aaa aaa 336
 Gln Leu Leu Lys Glu Met Asp Tyr Gln Thr Arg Arg Asn Ile Lys Lys
 100 105 110

aca tat gat att ggt gtc aaa act aaa acg tta acg att gat gaa acg 384
 Thr Tyr Asp Ile Gly Val Lys Thr Lys Thr Leu Thr Ile Asp Glu Thr
 115 120 125

caa act ttt ttc gac tta ttc cat atg gct gag gaa aag cac ggt ttc 432
 Gln Thr Phe Phe Asp Leu Phe His Met Ala Glu Glu Lys His Gly Phe
 130 135 140

aaa ttc cgt gag tta cca tac ttt gaa gaa atg caa aag tta tac gat 480
 Lys Phe Arg Glu Leu Pro Tyr Phe Glu Glu Met Gln Lys Leu Tyr Asp
 145 150 155 160

gac cac gcc atg tta aag ttg gcg tat att gat tta aac gag tat tta 528

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Asp His Ala Met Leu Lys Leu Ala Tyr Ile Asp Leu Asn Glu Tyr Leu
 165 170

aaa acg ttg caa tta
 Lys Thr Leu Gln Leu
 180

543

<210> 280
 <211> 181
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 280
 Arg Gly Pro Val Met Asp Tyr Thr Asn Gln Ser Leu Val Ala Phe Phe
 1 5 10 15

Phe Lys Ala Leu Thr Ser Tyr Leu Lys Lys His Asn Cys Leu Tyr Val
 20 25 30

Leu Val Asp Pro Tyr Leu Ile Glu Asn Leu Arg Asn Ala Asp Gly Glu
 35 40 45

Ile Val Lys Ser Tyr Asp Asn Arg Ala Phe Val Arg Thr Met Asp Lys
 50 55 60

Leu Gly Tyr Lys His Gln Gly Phe Pro Val Gly Tyr Asp Ser Met Ser
 65 70 75 80

Gln Ile Arg Trp Leu Ser Val Leu Asp Leu Lys Asp Lys Thr Glu Asp
 85 90 95

Gln Leu Leu Lys Glu Met Asp Tyr Gln Thr Arg Arg Asn Ile Lys Lys
 100 105 110

Thr Tyr Asp Ile Gly Val Lys Thr Lys Thr Leu Thr Ile Asp Glu Thr
 115 120 125

Gln Thr Phe Phe Asp Leu Phe His Met Ala Glu Glu Lys His Gly Phe
 130 135 140

Lys Phe Arg Glu Leu Pro Tyr Phe Glu Glu Met Gln Lys Leu Tyr Asp
 145 150 155 160

Asp His Ala Met Leu Lys Leu Ala Tyr Ile Asp Leu Asn Glu Tyr Leu
 165 170 175

Lys Thr Leu Gln Leu
 180

<210> 281
 <211> 1539
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1516)
 <223> RXN00165

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096308 : 062700

09E030B 0E770E0

gtt atg aaa tgagtgggga gacgtcgaaa agc
 Val Met Lys
 470

1539

<210> 282
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 282
 Val Ala Ser Ala Gly Met Ala Ala Ser Phe Ile Cys Asn Gly Leu Thr
 1 5 10 15
 Pro Val Ile Val Gly Lys Ala Val Asp Glu Ala Ile Gly Thr Ser Asp
 20 25 30
 Leu Gln Arg Leu Trp Phe Trp Ile Ala Met Leu Ala Val Leu Phe Leu
 35 40 45
 Thr Ala Met Thr Val Asn Trp Ile Ala Arg Tyr Met Leu Val Arg Ser
 50 55 60
 Gln Gln Leu Val Ser His Asp Leu Arg Met Leu Val Thr Asp Arg Ile
 65 70 75 80
 Gln Asp Pro Arg Gly Phe Ala Gly Lys Glu Arg Thr Ala Gly Gly Leu
 85 90 95
 Leu Ser Ile Ala Ser Ser Asp Thr Gln Arg Val Gly Asp Ile Val Met
 100 105 110
 Met Thr Val Phe Pro Val Ala Glu Leu Ala Ser Ile Ile Tyr Gly Ala
 115 120 125
 Val Val Met Tyr Ser Ile Asn Pro Trp Leu Ser Val Ala Val Leu Ile
 130 135 140
 Gly Gly Pro Leu Leu Val Val Val Ala Ile Gln Val Ser Lys Pro Leu
 145 150 155 160
 Gln Lys Arg Ser Gly Ala Arg Gln Gln Ala Val Ala Gln Ala Ala Ala
 165 170 175
 Thr Ala Thr Asp Val Val Gln Gly Leu Arg Ile Leu Lys Gly Leu Gly
 180 185 190
 Ala Ile Val Thr Val Arg Arg Arg Tyr Glu Ala Ile Ser Gly Glu Ala
 195 200 205
 Tyr Arg Lys Thr Val His Ala Asp Ala Ala Glu Ala Arg Leu Asn Gly
 210 215 220
 Val Thr Asp Ala Ala Gly Ala Ile Phe Val Ser Ala Leu Gly Ile Gly
 225 230 235 240
 Ala Gly Phe Leu Ala Leu Gln Gly Gln Met Ser Ile Gly Asp Leu Ile
 245 250 255
 Thr Val Val Gly Leu Thr Gln Phe Leu Ile Met Pro Met Thr Met Leu

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260
Gly Arg Asn Val Ala Ser Arg Trp Ala Ser Ala Glu Ala Ser Ala Lys
275 280 285
Arg Ile Arg Gly Val Leu Gly Ala Asp Phe Glu Arg Val Ser Ala His
290 295 300
Asp Ala Asp Lys Ala Glu Ile Ile Gln Gln Leu Ala Lys Gly Leu
305 310 315
Thr Val Ile Arg Gly Thr Asp Glu Gln Leu Val Glu Val Leu Glu Gln
325 330 335
Leu Pro Arg Thr Arg Val Ile Val Ala Pro His Ala Ala Asp Leu Phe
340 345 350
Asp Gln Ser Val Arg Asp Asn Val His Pro Val Ala Glu Val Ala Glu
355 360 365
Lys Ala Ile Glu Val Ala Ser Cys Asp Asp Ile Pro Gly Gly Ser Ser
370 375 380
Lys Ile Val Gly Glu Gly Gly Arg Leu Leu Ser Gly Gly Gln Arg Gln
385 390 395
Arg Val Ala Leu Ala Arg Ala Ile Ala Phe Asp Pro Glu Val Leu Val
405 410 415
Leu Gln Asp Pro Thr Thr Ala Val Asp Ser Val Thr Glu Gln Asn Ile
420 425 430
Ala Gln Gln Val Ala Ala His Arg Ala Gly Lys Val Thr Ile Val Phe
435 440 445
Ser Glu Ala Pro Ala Trp Ser Ala Val Ala Asp Gln His Val Glu Ala
450 455 460
Ala Ala Leu Arg Glu Val Met Lys
465 470

<210> 283
<211> 1470
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1447)
<223> RXN01190

<400> 283
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gcagcggggc aaggttgogt ttgggcgcatt ctttttgggg atg tgg cag ctg tcg 115
Met Trp Gln Leu Ser 5

gaa gca ttg gtg ccg att gcg att ggt ttg atc gtt gat cat gcg gtt 163
Glu Ala Leu Val Pro Ile Ala Ile Gly Leu Ile Val Asp His Ala Val

10										15										20									
ctc	aca	aaa	gat	ctc	cgc	cga	tta	gtg	gtc	ggg	ctt	gtc	gct	ttt	gtt					211									
Leu	Thr	Lys	Asp	Leu	Arg	Arg	Leu	Val	Val	Gly	Leu	Val	Ala	Phe	Val														
			25							30					35														
gtg	ctg	ttt	gtg	gtg	ttg	agt	ttt	tct	aat	cgt	ttc	ggg	tcg	cgc	gcg					259									
Val	Leu	Phe	Val	Val	Leu	Ser	Phe	Ser	Asn	Arg	Phe	Gly	Ser	Arg	Ala														
			40					45					50																
ttg	aat	agg	gcc	gtg	aac	ttt	gaa	tcc	cat	cgc	ctc	cgc	gta	gag	gta					307									
Leu	Asn	Arg	Ala	Val	Asn	Phe	Glu	Ser	His	Ala	Leu	Arg	Val	Glu	Val														
			55				60					65																	
gcc	gat	cat	cgc	ttg	aag	aat	ctg	gat	ccg	cgc	aat	ttg	gtg	cct	ggc					355									
Ala	Asp	His	Ala	Leu	Lys	Asn	Leu	Asp	Pro	Arg	Asn	Leu	Val	Pro	Gly														
			70			75				80					85														
gag	gtg	atg	tcg	cgg	tcc	acc	gca	gat	cgc	gat	tct	tcg	acg	cgt	att					403									
Glu	Val	Met	Ser	Arg	Ser	Thr	Ala	Asp	Ala	Asp	Ser	Ser	Thr	Arg	Ile														
				90						95					100														
ttc	ggg	cag	atc	gga	acc	ggg	gtt	tcg	gct	cgc	acg	gga	ttt	ctt	ggg					451									
Phe	Gly	Gln	Ile	Gly	Thr	Gly	Val	Ser	Ala	Ala	Thr	Gly	Phe	Leu	Gly														
			105					110					115																
gca	cgc	acc	tac	ctg	ttg	atc	agt	gac	tgg	ctg	gtc	ggg	ttg	ttg	gtg					499									
Ala	Ala	Thr	Tyr	Leu	Leu	Ile	Ser	Asp	Trp	Leu	Val	Gly	Leu	Leu	Val														
			120				125					130																	
ctt	gtg	ctg	gta	ccg	atc	att	tcg	gga	gtg	gtt	gca	ctg	gct	agc	aag					547									
Leu	Val	Leu	Val	Pro	Ile	Ile	Ser	Gly	Val	Val	Ala	Leu	Ala	Ser	Lys														
			135				140					145																	
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gct	ggt	att	ggt	gag	ttg	tcc	att	cgc	gtg	aat	ttg	gct	cgc	gtg	ttg					787									
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 Pro Ala Ser Thr Leu Pro His Gly Asp Asn Ile Leu Ala Thr Pro His
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 His Glu Asp Asn Val Pro Ile Asp Pro Gln Val Ile Arg Ala Ser Gly
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 Leu Thr Asp Ile Ile Glu Val Asp Gly Leu Asp Ala Pro Val Arg Asp
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agg gcg ttg cat gca gac gcg gaa gta ctg gtg ctg atg gat cca acc 1315
 Arg Ala Leu His Ala Asp Ala Glu Val Leu Val Leu Met Asp Pro Thr
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 Ser Ala Val Asp Ser Val Thr Glu Val Ser Ile Ala Gln Gly Ile Lys
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cag ctg cga gca ggc aaa acc acc att gtg gtg agt tct tcg ccc gcg 1411
 Gln Leu Arg Ala Gly Lys Thr Thr Ile Val Val Ser Ser Ser Pro Ala
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 Phe Gly Ser Arg Ala Leu Asn Arg Ala Val Asn Phe Glu Ser His Ala
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 Leu Arg Val Glu Val Ala Asp His Ala Leu Lys Asn Leu Asp Pro Arg
 65 70 75 80
 Asn Leu Val Pro Gly Glu Val Met Ser Arg Ser Thr Ala Asp Ala Asp
 85 90 95
 Ser Ser Thr Arg Ile Phe Gly Gln Ile Gly Thr Gly Val Ser Ala Ala
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 Thr Gly Phe Leu Gly Ala Ala Thr Tyr Leu Leu Ile Ser Asp Trp Leu
 115 120 125
 Val Gly Leu Leu Val Leu Val Leu Val Pro Ile Ile Ser Gly Val Val
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 145 150 155 160
 Lys Leu Ala Glu Ser Gly Ala Gln Ala Ser Asp Ile Met Met Gly Leu
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 Arg Val Ile Lys Ala Ile Gly Gly Glu Arg Trp Ala Val Lys Thr Phe
 180 185 190
 Glu Lys Ala Ser Gln Ala Ser Ala Arg Ala Ala Val Asp Thr Ala Val
 195 200 205
 Ala Ser Gly Lys Val Ala Gly Ile Gly Glu Leu Ser Ile Ala Val Asn
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 225 230 235 240
 Leu Gly Pro Gly Gln Leu Ile Ala Ile Val Gly Val Ala Val Tyr Leu
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 Ser Glu Pro Ile Arg Leu Leu Ser Asn Ser Ile Asn Ala Ser Ala Ile
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 Ala His Gly Ala Ala Glu Arg Val Ala Asn Phe Leu Asn Leu Asp Glu
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 Ser Gln Ala Gln Tyr Glu Ser Ser Glu Thr Ile Asn Asp Gly Glu Phe
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 Leu Val Ile Val Pro Pro Ala Ser Thr Leu Pro His Gly Asp Asn Ile
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 Leu Ala Thr Pro His Ala Ala Asp Ile Phe Glu Gly Thr Leu Arg Ser
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 Asn Ile Ser Met Asn His Glu Asp Asn Val Pro Ile Asp Pro Gln Val

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 Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly Val Phe Ile Gly Leu
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 Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala Leu Gly Asp Gln Phe
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 Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val Ile Ala Leu Val Ala
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gcg gtg atg tgt ctg cgt att ccg cag gtt aag gca gcg gca aag cag 643
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 Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val Ser Thr Trp Lys Leu
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 Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile Ile Gly Phe Leu Gly
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 Ile Phe Ser Val Glu Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg
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 Gly Ile Gly Phe Gly Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala
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 Glu Leu Val Pro Val Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly
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Phe	Glu	Leu	Pro	Thr	Ser	Thr	Leu	Met	Glu	Gly	Leu	Ser	Gly	Gly	Gln	
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Gln	Leu	Glu	Asn	Phe	Val	Gln	Gly	Leu	Arg	Gly	Gly	Val	Val			

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 Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln His Ala Arg Asp Gln
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 Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu Val Ala Arg Ala Arg
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 Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg Asn Ala Ile Lys Arg
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Arg Phe Ile Gln Ala Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met
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Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro Val Ser Gly Cys Pro
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Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala Pro His Thr Ile Glu
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Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln Glu Asp Trp Pro Glu
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Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu Val Asp Val Val Lys
90 95 100

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002200-002200

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 Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile Leu Ile Thr His Asp
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 Pro Gln Lys Val Ser Val Arg Asp Leu Val Thr Ala Val Ala Glu Val
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00603200.062300

50 55 60

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1 5

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Lys Met Cys Gly Met Asn Pro Asp Ser Gln Tyr Val Glu Leu Ala Val
10 15 20

gaa gtt ttc gga ctc ctc gcg gac gcc act cga gtt cgc atc atc ttg 211
Glu Val Phe Gly Leu Leu Ala Asp Ala Thr Arg Val Arg Ile Ile Leu
25 30 35

gca ctt cga aac agt ggt gaa ctt tcc gta aac cac ctc gcg gac atc 259
Ala Leu Arg Asn Ser Gly Glu Leu Ser Val Asn His Leu Ala Asp Ile
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Val Asp Lys Ser Pro Ala Ala Val Ser Gln His Leu Ala Arg Leu Arg
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70 75 80 85

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Lys Leu Thr Asn Glu His Ala Ser Gln Leu Val Ser Asp Ala Ile Phe
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20

09603208-062300

APPENDIX B: Amino Acid Sequences

> RXA00062 (1-1398, translated) 466 residues
 MILSIVVLGY FMILLDTISV ITGLPAIGSE LGIDPVHLSW VQSSYTLVFG ALLLLGARAG
 DIFGRKKVLY IGLALFAASS LAIALSPNAA VLIGARVVQG AGAAIIAPAT LALITEFFPE
 GPARLRATSA YGAVAGIGVA AGLVIGGVFA DLLSWRIGFV INVPIAAVLA YIVHKAIPAT
 FSRPGSLDIF GAITSTAGIA AVLVAIVRSA DYSWTDPFVL ISLVLGIAVF IFLRHESHA
 KEPLLPLGLF KNRRRNTILA SRFLLVGSVM SFFFFATQLF QDTMGMNALQ AGLAFMPLSL
 LQFASAAAMPV RLSRAGVSDS MLTVIGFAIM VIGMAGLAFV PNTMIALILP IULVVGQGF
 AFGPMTALAV QGAPKQSGA VSGLVNSLHQ IGGTFGLGVF SSLAVAVIGH DATSEMISDR
 AHFGFLLSTV TLTLATIFAV TLLKRHETRK SSERPQLVD EKAVTS

> RXA00084 (1-825, translated) 275 residues
 MSTALPDQLK WEYSAFPVQI SQKQRLSPGF MRITVTGDKL RFFGQWGLDQ RIKLIIPSPA
 GNIPDFGILD EPTPPPTTWL PRAKSFPAQ RPILRTYTSP AVRPELCEVD IDIYLNHPSG
 PVSRRWAKNCS VDDELIITGP DVRAGETGYG IYHYPTSAID RLCLIGDCAS APAATANVNO
 SKVPTTFLH VDSLEDDVLI ADSSTKLTFE DIDAYKAKVF QWASANAADP SVHFWIAGET
 SMVRFIRKEL INSYRVDSSR ITFLGYWKYG RRTVD

> RXA00109 (1-612, translated) 204 residues
 VASEKNLKLRL TLAAGAAGVLG VGAMSMVLVAP QAAAHDVVDV SNPENGSVVD EFPETIELEF
 SGIPQDLFTT VALSNADSGE VLTSGTPQLE GQHLSEYVPS DVQGTAGNYI LGFQITSSDG
 HATKGSISFE VTGSAETITE TTAETTTESA ATTDSTETTE AETTETADET SGIPAPWNNV
 LSTVAVLVVA SAIVMMIAKN RNQK

> RXA00215 (1-1461, translated) 487 residues
 VSDKKQDITS SAAGSAAPQT KAYPAMPLPE KQAWPALIAL CIGFFMILLD QTIVAVSTPA
 LQADMGASYN EWIWVTSVYL LTFAPVLLVT GRLGDKYGPV NVYVAGMVIF TVSSLACGLA
 PDMFTLIIAR GVQGLGAALL TPQTMATINR IFAEFERRGAA LGVWGSTAGL ASLAGPILGG
 VITENMGWQW VFYINVPIGV ISVIAVMKYV PEFFPLTRPL DPLSIVLSIV AVFLLVFAFQ
 EGEAGGWAAP WIMIVAAFA LFAWFIYQQS RAEKSGNDPL VPLEIFKERN FSLGNICIMA
 MGTVTAGTPL PIMLYFQQAQ GMNAMEAGFM MVPQALMAAV LSPFVGKLMVD RSNPGLMAAL
 GFSTVAVSIV LLSVMVIFDT GLVWALVSMT LLGIGNAFVW APNSTSTMTR LPHKFMAGAS
 GVNTTTRQLG SVIGAAAIQA VMQIRLAAGD EGAAFGQALL LAALVLVIGI VAPMTAGKNA
 HPAPVKP

> RXA00289 (1-1176, translated) 392 residues
 MSTTTAPEAR FPVPLTAMS FAFVYVTFE MFAVGLIKPM ASDLGVSESS IGLLMTVYAT
 VVAVVTIPAM LWSRFNKRT VFLITLAFLA TGIIVQVALT NYGMLAIGRT IAALTHGVFW
 ALVGPMAARM SPGHTGRAVG VVSIGSTMAL VVGSPLATWI GELIGWRPAT WILGALTIAA
 VAVLIPTVPS LPPLPDTESE SKEKKSLPWG LLSLVIFLL AVTGVFAYAT YLGLIIAETA
 GDSFVIGLGF AFGALGLIGV TVATRTVDQR MLRGSVHTT LFVIAAILGQ AFLGLEGTIA
 VVAIFLAVTV FGGAYGALPT LGTTIFLHAG RDHPDTASSI YVVTYQVGIA SGAAALGAMAV
 DADWVAGTLW IMAGLSLAST LALALWSRPL LK

> RXA00404 (1-2316, translated) 772 residues
 VALKRPEKKT VKIIVIKQTD NINDDDLVYS NATDLPGVVK KSPKMSPTAR VGLLVFGVIA
 AVGWGAIAFS RGETINSVWL VLAAGVSYII AFSFYARLIE YKVVPKPKDQ ATPAEYNDG
 KDVPITDRRV LFGHHFAAIA GAGPLVGPVM AAQMGLPGT LWIILGVIFA GAVQDYLVLW
 VSTRRRGSLG GQMVRDEMGV VGGAAGILAT ISMIIITAV LALIVVNALA DSPWGVESIT
 MTIPLALFMR VYLRYLRFGR VTEVSIIGVA LLLLATVAGG WVADTSWGEW WFTWSKTTLA
 LALIGYGIMA AILPVWLLLA PRDYLSTFMK IGIVGLLAVG ILFARPEVOM PSVTSFALEG
 NGPVTSKGLF PFLFITIACG ALSGFHALIS SGTTPKLVEK EQSMRMLSGV GMLMESFVAM
 MALITAVILV RHLFYSMNAP LALTGGDPAT AAEWVNSIGL TGADITPEQL SEAEASVGES
 TVISRTGGAP TLAFGMEIIL SGFIDGAGMK AFVYHFAIM EALFILTTVD ACTRVARFVM
 TDILGNVPGL RRFKDPSSWTW GNWISTVFCV ALWGAILLMG VTDPLGGINV LFPFLGIANQ
 LLAATALALV LVVVVKGLY KWAIVPAVL AWDILVMTA SQMKIFSHD AIQWAGNANQ
 FRDAKSQGLT EFGAAKSPEA IDAVIRNTMI QGLSLILFAV LVLVVVGAAI AVCIKSIRAR
 AGTPLETTE EPTDESEFFA PTGFLASSRD KEVQAMWDER YPGGAPVSSG GH

> RXA00479 (1-2190, translated) 730 residues

MSTSITTEENK KKSQPPRLMR IFLPALLILV WLVGAGVGPP YFGKYSEVSS NSQTTYLPES
 ADATQVQEQQL GDFTDSESIPI AIVVMVSDEP LTQDDITQLN EVVAGLSELD IVDSEVSPAI
 PSEDRGAVQV FVPIPNPSAEL TESVEKLSET LTQOTPDYVS TYVTGPAQGT ADLSAFAFI
 DGLLLAVALA AVLVILVIVY RSFILPIAVL ATSLFALTVA LLVVMWLAKW DILLSSGQGT
 GILFILLVIGA ATDYSLLIYA RFREELRVQO DKGATGKAI RASVEPILAS GSTVIAGLLC
 LLFSDLKSNS TLGPVSAVGI IFAMLSALT LIPALLFVFGR VAFWPKRPKY EPEKARAKND
 IPASGIWSKV ADLVEQHPR A IWVSTLIVLL LGAAVFPTLK ADGVSQSOLV LGSSSEARDGQ
 QALGEHFPFGG SSGSPAYIIVD ETQAAQAADV VLNNDNFETV TTSADSPSG SAPITADGIV
 PLGSGTAPGP VVVEGQVLLQ ATLVEAPDSE EAQKAIARSIV QTAFADENISA VVGVTATSV
 DTNDASIHDR NLIITPIVLLV ILVILMLLLR SIVAPLLLVV TTVVSFATAL GVAALLFNHV
 SFSFGADPAV PLYGFVFLVA LGIDYNIFLV TRIREETKTH GTRLGILRLG VTGQGVITSA
 GVVLAATFAA LYVIPILFLA QIAFIVAFAV LIDTLVRAF LVPALFYDIG PKIWMPSKLS
 NQKYKQKQPL

> RXA00497 (1-297, translated) 99 residues
 VANVNKIFLE DKILVQINEA ETTTASGLVI PDSAKEKPQE ATVIAVGPGR FDDKNRIPL
 DTKEDDVVIF SRYGGTEIKF GGVEYLLLSA RDILAIVEK

> RXA00498 (1-1239, translated) 413 residues
 MAKLIADFQD AREGILRGVD ALANAVKVTL GPRGRNVVLD KAFGGPLVTN DGVTIARDID
 LEDDPFENLGA QLKVSAVAKT NDIAGDGTMT ATLLAQALIA EGLRNVAAGA NPMELNKGIS
 AAAEKTLEEL KARATEVSDT KEIANVATVS SRDEVEKVGKD GVVTVVEESQS
 IETALEVTEG ISFDKGYLSP YFINDNDTQQ AVLNDPAVLL VRNKISSPLD FLPLLEKVV
 SNRPILLIAE DEVEGEPLQTL VVNSIRKTIK VVAVKSPYFG DRRKAFMDLD AIVTKATVVD
 PEVGINLNEA GEEVFGTARR ITVSKDETII VDGAGSAEDV EARRGGIRRE IANTDSTWDR
 EKAEERLAKL SGGIAVIRVG AATETEVDNR KLVRVEDAINA ARAAAQEGVI AGG

> RXA00565 (1-993, translated) 331 residues
 MMLNLTTLAV ALPSIMADF IEANTAQWLL TGFMLTMAVV LPATGWMLER FTTRSVPFIFA
 TVVFLIGTGT AALSPTFAIM LAARVAQAVG TAVIMPLMT VAMTVVPPER RGAVMGLIAV
 VMAVGPAALGP SVAGFVLSLS SWHAIFVWV PLFVVASLIT TLRLTNVSEP KKTPLDVISF
 LISAVFTGGL VYLLSSIGII LEGDRSALVV LAVGIIALVV FVWRQIATMGK QDKALLDLRP
 LAIREYTIPL VALLTLFGAL LGVMNTLPLY LQGSMLMTAL VAGLVLLPGP LLEGVLSPFV
 GRIYDRHGPR GLVIGGMSLV VISLFASTV D

> RXA00575 (1-483, translated) 161 residues
 VRDIYELGLE TGHATYETSG PTWQQFSQSK IMDTVMWAVE NNDPDFILCW VSAAPISSRQ
 VFHGVEDSI YIHPQGGQGR IGGALLDALI TYCESNGIWS IHSWIFFENL GSAKLHESKG
 FVKVGTMHQM ARMPYGEEMG QWRDCDLWEC LLSVPEQAQS S

> RXA00599 (1-387, translated) 129 residues
 MKSVLFVCVG NGGKSQMAAA LAQKYASDSV EHSAGTKPA QGLNQLSVES IAEVGADMSQ
 GIFKAIDPEL LRTVDRVVIL GDDAQVDMPE SAQGALERWS IEEPDQAQME RMRIVRDQID
 NRVOALLAG

> RXA00600 (1-1098, translated) 366 residues
 MIEGWMLTTL KEHSTPRAAG SMSFLDRWLA AMIFLAMAAG LLIGKVFPPI GALLSAVEIG
 GISIPAIAGL IVMYTPPLAK VRYDKTKEIS TDRLMNVVSI MLNWIIVGPAL MFSIAWLFLP
 DQPELRTGLI IVGLARCIAM VLVWSDLACG DREATAVLVA INSVFPQILMF GVLGWFPYLI
 LPSWLGDLDT SVTFESVSVIV TSVLVFLGIP LVAGVLSRVI GEKTKGRRY EDTFPLKPSI
 LALIGLLYTI VLLFSLQGD EITAQFWTVAR LALPLLMYFV GMFFISLVVS KLSGLTYERA
 ASVSTAAGN NFELAIAVSI GTFGATSPQA LAGTIGPLIE VPIVLVLVY MLWLGPKIFK
 KENAGS

> RXA00605 (1548, translated) 516 residues
 MSEKSAADQI VDRGMRPKLS GNTTRHNGAP VPSENISATA GPQGNVLND IHLIEKLAHF
 NRENVPERIP HAKHGGAFFE LHITEDVSEY TKADLFQPGK VTLAVRFTST VAGEQSSPDT
 WRDVHGFALR FYTEEGNYDI VGNNTPTFFL RDGMKFPPDFI HSQKRLNKG LRDADMQWDF
 WTRAPESAHQ VTYLMGDRGT PKTSRHQDGF GSHTFQWINA EGKFPVWKYH FFKTRQWDCF
 TDAEAAKAVG ENADYQREDL YNAIENGDFP IWDVKVQIMP FEDAEINRWN PDLTKTWSYR
 KDYPILIPVY FILNRNPRNF FAQIEQLALD PGNIVPGVGL SPDRLQARI FAYADQQRYS

00602990-00603000

IGANYRDLVP NRPINEVNTY SREGSMQYIF DAEGEPSYSP NRYDKGAGYL DNGTSSSSNH
TSYGQADDIY VNPPDHGTDL VRAAYVKHQD DDDFIQPGIL YREVLDEGEK ERLADNISNA
MQGISEATEP RVYDYWNNVD ENLGARVKEL YLQKKA

> RXA00648 (1-1410, translated) 470 residues
VVTLASAGIT VSLAQTLVIP IIGRLPEIFN TTAANASWII TVTLVLGAVA TPVMGRLADM
YGKKKMMMLIS LVPPFILGSL CAVSVDLIPM IIGRGFGGLG SGLIPLGISL MHDLLPREKA
GSAIALMSSS MGIGGALGLP LAAAIQAQFS WRVLFWFTAL VALTVGAVIN KAIPARPRIV
RSGGFDYFGA LGLAMGLIAL LLAVSKGSEW GWSALTIGL FVAALVILVG WGWFPETROKS
PLIDLRTTIR ATVLMNTIAS ILIGFTMYGM NLILPQVMQL PVILGYGLGQ SMLQMGIWLI
PMGLGMMMLIS NAGAAISAHA GPRVTLTIAG VVIAVGYALT ATVLFTIGNR TPGGDADNAL
ILTTLVLFVS CSLVVVGIGI LAFGSMPALI MGAVPATEKA AANGFNSLMR SLGTTGSSAV
IGAVLAGMMS GGVPTLGGFM TTIIIGCCAA LVAAVISYFI PTTTTVVEAK

> RXA00764 (1-1116, translated) 372 residues
MTLKTSVLAL LLDNVHVLII ANPESTTQTQ KLFRRVVPAL MALDGVSLAE RFTHYGGHAE
EMVAGLTVDL FVDIIPAGGD GTVNEVINGL LGSAGGDFRN LEDLPAIAVL PTGSANVFAR
ALGYPTDPYA AADALVELIR KNRTRITILG TWKGDDQGRF WFAVNAGFGI DADVIAVER
ARSGFPAASP LLYLQVSLRA WVKTQIKPPK ITVEAVDSKG HKLQKEEVPV LLASNTNFWT
FLGPLPVVTN PQNSFDTGLG LFGLTSVRGF GGVAAMMHIL GVGHGRKLEK LIAKRTIAFD
DAEKVTLTCD SQRFQVDGE YEGKPTKVVL ESITDAVRVY APKTHPTPPI MNWAVHLEFKH
VRDFLRVTFE GI

> RXA00803 (1-603, translated) 201 residues
MGVSALNMSD MVANKRAQRK VMLAVALSVF TVAWGGNEFT PLLVFYRGEG FFSNLFIDLL
LVFFYAGVAV GLLAAGPLSD RYGRRAVMP LPLAILGSA LIASGEETAI LIAIGRVLSG
ISVGMVMTAG GSWIKELSSS RFEPGVKTSR AKRASMSLT GGFALGPALA GVMAQWLPOQ
GQLAVVLHII LTLILFPLLI T

> RXA00810 (1-201, translated) 67 residues
MAQGTVKWFN PEKGFGFIAP SDGSADVFEH YSEIEGNFR TLEENQLVEF EIGEGAKGLQ
AQAVRAI

> RXA00829 (1-255, translated) 85 residues
LDEPTTGLHL ADVKTLLDLF DQLVDDGKSV IVIEHHLGLV AHADHIIDVG PGAGSDGSGI
VFEGSPAELI KTDTPTRHRL KAYVD

> RXA00834 (1-1563, translated) 521 residues
MQKADSHDWI SVHGANENNL KNVSVRIKPK RLTVFTGVSG SGKSSLVFGT IAAESRRLIN
ETYSTVFQGF MPMSARPVDV HLEGITTAII VDQEQMGANP RSTVGTATDA TAMLRILFSR
IAEPNAGGPG AYSFNVPVS ASGAITVEKG GNTKREKATF KRTGGMCPAC EGMGRASDID
LKELEFASLS LNDGALTIPG YTPGGWSYRM YSESLGFDAF KPIKDFTEEE RHNFLYLEPT
KMKIAGINMT YEGILPIRQK SMLSKDREGM QKHIRAFVDR AVTFIPCPAC GGTRLAPHAL
ESKINGKNIA ELCAMEVRDL AKWIKTVEAP SVAPLLTALT ETLDNFVEIG LGYIQLDRPA
GTLSGGEAQR TKMIRHLGSA LTDVTYVFDE PTAGLHAYDI ERMNKKLLDL RDKGNTVLVV
EHKPTETIAA DHVVDLGFGA GAGGGEIRFE GSVDKLKDSI TVTGLHFNDR ASLKESVRAP
HGALEIRGAD RNNLNNVDVD IPLGVFTAIS VGAGSGKSSL I

> RXA00843 (1-345, translated) 115 residues
MKVTIFHNPR CSTSRNTLAY LRDKDIEPEI VQYLKDTPTA SELKELFNLT GIPVHDGIRT
RKEAYTEGLG SPETPETELI DAIVAHPRLL QRPIVVTARG ARIARPKIDV IDSIL

> RXA00858 (1-468, translated) 156 residues
MEVNLATWLI TIAVIAGFFI FDFYSHVRTP HEPTIKESAW WSLFYVALAC VFGVFLWFAM
GEPGNPHQHG IEFFTGYYTE KALSVDNLFI FALIMGSFKI PRKYQQKVLL IGIALALVFR
LAPILAGAAV IEAWSDFYFI FSIWLIYTAV KAPVHE

> RXA00886 (1-1146, translated) 382 residues
VARDYYGILG VDRNATESEI KKAYRKLARK YHPDVNPGEE AAEKFREASV AHEVLTDPPK
RRIVDMGGDP MEQGGGAGAG GFGGGFGSGG GLGDIFDAFF GGGAGGSRGP RSRVQPGSDT
LWRTSITLEE AYKGAKKDLT LDTAVLCTCK HSGSGASDKK PVTGCGCNGA GEIQEVQRSF

09603208.062300

LVGNMSTRPC HTCDGTGEII PDPCTECAAD GRVRARRDIV ANIPAGIQSG MRIRMAQOGE
 VGAGGGPAGD LYIEVMVRPH AIFTRDGGDL HASIKVPMFD AALGTDELVE SLTGEEVKIT
 IPVHGQPNVD ITLDGEGMPK LRAEGHGNLM AHVDLFVPTD LDDRTRELLE EIRNHRSDNA
 SVHREGGEES GFFDKLRNKF RK

> RXA00900 (1-852, translated) 284 residues
 VRGIARAIVP DLERGQKAAH AFALLMIIQG IAPVVAFLIG GVLVGFPGWR GIFWALALVN
 FAQLLVALLO IKESKPVVEER TAAGLGGMLS NYVFLVKNPQ FLAYVFTLGL SFGAMFSYIS
 ASPFVLQNM GLPVLLYSII FGVNAFLGIV GGMVNRLLQ RIHPHRIMQT VLASFTVLCA
 LLLIEVLFIN WIFLFLLLF LIVSHIPVM ANATALGTEV VRSRAGSGSA ILGFVQFTMG
 ALVSSLVGLG SDKALTMGIA MTACALLACG CAYLAGRGI PEMK

> RXA00901 (1-378, translated) 126 residues
 MGLALLSASS ALATDMYLPA MPGIAEDLGT TAPMVQLTSL SFGAMAGIQ LIIGPLSDQL
 GRKGLLVAGA VAALVASVVC ALAPSISVLV IARLVQGLGG GACVVLRRAS CQTINADKRL
 RTPLHC

> RXA00981 (1-630, translated) 210 residues
 MSENLPAPEN LLDAERIQMI KNFRNELTGF MLNYQFGIDE ILTKINILKT EFSQLHEYAP
 IEHVSSRLKT PESIVKKVIR KGDELSLAAI KDTVFDIAGI RIVCSFLKDA YAIADMLTNQ
 KDVTVIEAKD YIANPKPNYG KSLHLILQVF VFLSNSVEKV NVEVQIRITIA MDFWASLEHK
 IYYKEQEVF SLDILDESLD GKNPRGSEVT

> RXA00993 (1-636, translated) 212 residues
 MGKGTGAIL TVMGVKSHIA TTTGKTVIND RMVTIHFHSE TLLNTEGEVP GDWLRLWFPH
 ESRPGKLYQR AYTLTNVDAD ACTFDLAFVL HEPLGPASAW ATRCAGESEL EVMRYPGIFP
 AIPDPAPRGF LPLGLDLSYP AICSILETLD GEIPATAYLI AHDPLDYTFD FPQGEHITAQ
 WISNQSQFID HIADTDYTFD YTWIGAESSE TR

> RXA00995 (1-741, translated) 247 residues
 MNPHYLLATV KRVLQLKAD KRSLALILLA PVALMSLFY MYSSPTAGTO LFKTISTVMI
 AVEPLMLMFL MTSVTMQRER NAGTLERLWT TNHVRVDLIG GYGVAFGIMA VAQSLMLVLT
 LRYLLGVETE SEWWISTLIA AITGLIGVSL GLLSSAFAT EFQAIQTLPL LILPQFLLCG
 LLIPRDDLPD VLRWVSNVLP LSYAVDAALE ASRTGIGQQV VVNIACAF AVSFLVLAAL
 SMPRMTR

> RXA00996 (1-741, translated) 247 residues
 MSTVTAVQVN GLKVSISGF SRKKTITILH DLDFTVETGK ITGLLGPSGS GKTTLMRAIV
 GVQNFDTGLE VFDQPAAGAS LRKGIGYVTQ NASVYHDLVS IENLKYFGAL AKGTSTPTTP
 EKILEVLIDIA DLAQKQVSTL SGGQGRVSL GCALIASPEL LVMDPTVGL DPITRQALWE
 EFTTIKAGA GVVISHVLE EAARCDNLIL LRDGRIWRG TPTRLLEDTG KSSYEDAFIA
 AIDGVR

> RXA01010 (1-771, translated) 257 residues
 MKKLQMPAIL VGGFVGPFTH QALSIVLPEF ADTFDISVSQ AALTMTAYLL PFATMMLFSG
 RTRIKIHPKH VQQAAYIVTL PLALLLVTP SWGLFMAAYA TIGIANAFT FLVQIMLREL
 VPPRSLGKAL GTYAAQSLG MLSAPLIAGV SSVVSWRLTF LVTAASLFI LVARLVPVVP
 PSALKQNVSG KQVWGPTIHH MVSGFVVIG IIGIGFMTSL HVGEQFGLMT AARGLVVMCG
 GRAAFFASRK IGDLDADK

> RXA01051 (1-609, translated) 203 residues
 MSTIHASGIG APQVPHGSHH APPQKDESVK KSFNASSLLF AFSFGVYLVL LVMMTLKSR
 LSLGGLWNTA AHQYRSIDLE LPNGFADPPI WGWPTNTFTG NIALFMPFGF FLYKMLRRFL
 HRFPFVETIL FASVTSLSIE VLQWVFAIGY SDVDDLLFNT IGLIGASVA ALVSLKSSKV
 VSGIIMGSSL SVMAMMYSS FIA

> RXA01052 (1-309, translated) 103 residues
 MDTKLGAELG TEFDLIVVGF GKAGKTIAMK RSAAGKRVALL IEQSPQMYGG TCINVGCIPT
 KKLFLFETATG KDFPDVAVAR DQLIGKLNK NLAMATDKGV TRH

> RXA01053 (1-420, translated) 140 residues

VLVYPTIVIN TGSTPVPINPV PGTDNPHVFD STGIQHISPL PKHLAIIGGG PIGLEFATLF
SGQSKVTII DRGELPLKNF DREVAELAKT DLEARGITFL NNAELTGFSG DLTIALKDHD
LLADAALFAS ADARHRRARP

> RXA01054 (1-489, translated) 163 residues
VLVDAHLRTN IDGIFAVGDV NGGPQFTYVS YDDHRIVLQD LAGTGKKSIA HRLIPTTTFFI
EPPLSTIGDN TEGENVVVKK ALIADMPFIVP RPEIINQPHG MVKFFVDKQS DALLGATLYC
ADSQELINTV ALAMRHGVTA SELGDGIYTH PATSEIFNQL LGS

> RXA01150 (1-891, translated) 297 residues
PAASLPALVA VRFVHGFSYS LASTAVMALV QSVIPASRRA EGTGYFALGS TLATAFGPAI
ALGIFIDDFNV NTFLEWITTAT SVFGLILTVL IRKPEFIKNA EHGVRKPVWS IKTVVHPSPVM
LIGFFMLAVG LAYAGVITFL NGFAQDGTGLT AGAGLFFIAY AVAMLVMRFF LGRIQDKHGD
NPVIYFGLIS FALALGLMAL ATEDWHIVLA GALTGLGYGT IMPAAQAIAY DSVPSQTQVGS
GISTLFLFTD IGIGLGPILL GGLVAATGYN VMYAALAAVI VVAGVLYLVA LGRKASH

> RXA01180 (1-762, translated) 254 residues
MTPTLASMIG LAVGIDYALF IVSRFRNELI SQTGANDLEP KELAERLRMT PLAARAHAMG
MAVGTAGSAV VFAGTTVLIA LVALSIINIP FLTVMIAIAA ITVAIAYLVA LSFLPALGLG
LGTRIFAARV PGPKVPDPED EKPTMGLKWV RLVRKMPVAY LLVGVLGLGA IAIPTATNRL
AMPTDGTSTL GTAPRTGYDM TADAFGPGRN APMALIDAT DVPEERPLV FGQAVEQFLN
TDGVKNQAQT QTE

> RXA01217 (1-600, translated) 200 residues
MAKYQTIEAA VRSEFGKGS RARVAVQIIP AVVYGADVES NLHVTIDHRT FAALVRQEGV
NAVLELDIEG QKQLTMIKHI DQNVLTFFHD HLDLLAIKRG EKVEVDVPVI VEGEPAPGTM
WVQDATTIKV EADVLSIFEE FTVSIEGLEL GAQITAADIK LEGDTTLVED PETLIVNIVL
PAVEEEDTEE DEAAEEAATE

> RXA01314 (1-741, translated) 247 residues
MTSQVKPDEE RPTVTISKSG APSAHTSAPY GAAATEEAVE EKTGKRVGFI IAAALMLALL
SSLGQTIFGS ALPTIVGELG GVNHMTWVIT AFLLGQITSL PIFGKLGDQF GRKYLFMFAI
ALEVVGSIIIG ALAQNMSTLI VARALQGIAG GGLMILSQAI TADVTTARER AKYMGIMGSV
FGLSSILGPL LGGWFTDGPW WRWGLWLNVP IGIIALVAIA VLLKLPARER GKVSVDWLGS
IFMAIAT

> RXA01319 (1-1194, translated) 398 residues
MTHETSVPGP ADAQVAGDTK LRKGRAKKEK TPSSMTPEQQ KKVWVWLSAL MVAMMASLD
QMIFGTALPT IYVGLGGVDH MMWVITAYLL AETIMLPYIG KLGDLVGRKG LFIGALGIFL
IGSVIGGLAG NMTWLIIVGRA VQGIGGGGLM ILSQAIADV VPARERGRYM GVMGCVFGLS
AVLGPLLGGW FTEGPGWRWA FWMNIPLGII AIGVAIYFLD IPKKSVKFRM DYLGTFEEMV
AATSILFHTL WGGSGYEWSD PIIGLIIT IVAAALLVNV ELRAKOLPLV MSFFQNRNFT
LTTIAGLILG IAMFGIIGYL PTYLQMVHGI NATEAGYMLI PMMVGMGMS ITWGIRISNT
GKYKLEFPPIG MVTTFVALIF FARMEVSTTL WQIGIYLF

> RXA01320 (1-780, translated) 260 residues
VDPLVPMGLF SNRNEVLTA AGIGVGLFMM GTIAYMPTYL QMVHGLNPTQ AGLMLIPMMI
GLIGTSTVVG NIVSKTGKRY WYFPIGLMIM VLALVLLSTL TFSASALIG LYFFVVGFLG
GCAMQILVLI VQNSFPITMV GTATGSNNFF RQIGGAVGSA LIGGLFISNL SDRFTENVFA
AVASMGEEGA QYASAMSDFS GASNLTPHLV ESLPQALREA IQLSYNDALT PIFALTPIA
VVAAILLFFI REDHLKETHE

> RXA01345 (1-1167, translated) 389 residues
MRFGDLGTT RTIAAAVDRG NYPIVTVEDS LGDTHDFIPS VVALKADRI AGWDAIEVGQ
DHPSFVRSFK RLLSEPNVTE ATPVYLGHDV HPLGAVLEAF AENVVYALRA FQTQLGDTSP
IEVVIGVPAN SHSAQRLLTM SAFSATGITV VGLVNEPSAA AFEYTHRRAR TLNSKQRAIV
VYDLGGGTFD SSLIRIDGTH HEVVSSIGIS RLGDDDFDEI LLQCALKAAQ RQHDFAFGKRA
KNITLDES RN AKEALVPQSR RLVLEIGDDD ITVPVNFYFE AATPLVEKSL SIMEPLIGVD
DLKSDIAGI YLVGGGSSLP LVSRLLRERF GRRVHRSPPF SGSTAVGLAI AADPSSGFFH
RDVARGIGV FREHDSGRAV SFDPLIAPD

> RXA01407 (1-891, translated) 297 residues
 LQDTIGCRWI FLLNVLPGII AIMAGLFQIP KNTAVNVKRF DRPGFLGAML VMVAQAVIAE
 LICSRSPAL TICACLVLSA AVVCGFVVRW LRVPGRLFDL SIMRIPGPRV GNSSGSIYRL
 VITAAPMET LFFQVAFGWS ATLAGAMVVA LFAGNVAIKP FTTPIIKRW FKPVLVFSNA
 AGAIVLATFL FVRADTPLVL IVLLLVVSGA LRLSGFSAYN TLQFVDISPE QTSNANVLSA
 TLHQLGMSLG IAVAVIAMS L APTANWAFPL AALFLIPLI GALSPLPRDG ARAFSSS

> RXA01408 (1-201, translated) 67 residues
 MRNDRSFSVP TALLAAGALF LEILDGTILT TAVPAIARDP GIDAVDVSLA LVAYLAAAAA
 GIPLQGG

> RXA01524 (1-1443, translated) 481 residues
 MDSQINTQS PAAAKLPREV VVLSILVVS AMIMINETI LSVALFSIME DFSVPETTAQ
 WLTTGFMILT AVVIPTTGYL LDRFSTKTIF VTALLFETVG TLTAALAPFIV AVLLGARIVQ
 AVGTALVMP LMTVTLTVVP AERRGSMGI ISIVISVAPA LGPTLSGVL NSLTWHWLEW
 MMLPIVVIAL VIGFFLIKNI GETKITPLDV LSVILSVFAF GGLVYGFSSF GALEGEGTV
 GIFAIIVGAI ALLIFALRQH QLGKQDKALM DLRAFVKVRNF SPSLTITILLA FGAMLGTVMV
 LPIYLTSLG VITALVTGLV MPGLLQGLI SPFIGRFYDK VGRPRLLIPG AIALAIAASS
 MTFLENLSPV VMVVVMHVVF SIGMCLMMTP LMTTALGALP KHLVGHGSAI LNTFQQLAGA
 AGTAIMIAAL SFGTSIAASS GSAHAEEAVAA GTRKVAFIAGA IIAVALLVVS LFVTRVEEEA
 H

> RXA01578 (1-1395, translated) 465 residues
 MTAALVAVFA FQLNASMLAP ALATMETELN ATAAQIGMTQ TAFFTAALAF SLFLPRWGD L
 IGRRKVLVGM MIVTGIGCVV AAFAPNVITL FLGRLLQGVV GPTVPLCLII LRQQVTNEKQ
 YALLGLIVTS VNGGIGGVDA LAGGWLAEFL GFRSIFWVMA AFCAVALALP PFSVKHSTAE
 ETPKMDWLG V LPLAVSIGSL LMAFNEAGKL GAANWILVVV LFIIGIAGVI FFYNTKEKRV
 HPLVSVYELG QRRTWALLLS TLLTMTGVFA VMNGLLPNLA QDAANGAGMS ASVSWWTLT
 PYALAGLVFG PIAGILAGKF GYKIVLQIGI AATIIGVAGA TFLVGSSTHL AYLIGSIFVG
 IYTAGIANIM LNLGIVLSP ANNOGYLPGM NAGAFNLNAG ISFAILFAVS TAFSDNGGGY
 AAGMWAGVII LVLAFLCSLL IPRPESITDT VAAKVQAEAA AQAA S

> RXA01616 (1-1482, translated) 494 residues
 MTSETLQAQA PTKTQRAWFL AVISGGFLFI GVDNSILYTA LPLLREQLAA SETQALWIIN
 AYPLLMAGLR LGAGTLGDKN GHRRMFLMGL SIFGIASLGA AFAPTAWALV AARAFLLIGA
 ATMMPATLAL IRITFEDERE RNTAIGIWGS VAILGAAGFP IIGGALLEFF WWSGVFLINV
 PVAVATIALT LFAVAPANIAN PSKHWDFLSS FYALLTLA GL ITIKESVNT ARHMLLLGA
 VMILIIIGAVL FSSRQKIEE PLLDLSLFRN RLFLGGVVAA GMAMFTVSG L EMTTQSRQPL
 SVGFTPLEAG LLMIPALGSL FPMIIGGAN LHRWGFKPLI SGGFAATAVG IALCINGATH
 TDGLFFFIAG LFFMGAGAGS VMSVSSTAI I GSAPVRKAGM ASSIEEVSKE FTGLLSVAIL
 GSLFFPFYSL HAPAEVADNF SAGVHHAIDG DAARASLDTA YINVLIIALV CAVAAALISS
 YLFRGNPKGA NNAH

> RXA01666 (1-1377, translated) 459 residues
 VSTFHKKVLN TMISNVTGTF LFFAVVFWMY LSTGNVALTG IVSGIYMGLI AVCSIFFGTV
 VDHNRKSKVM LFSSVTTLVF YCLSAVWVF WLEEDGLSIG NTA LWVVSF IILIGSIVEHM
 RNIALSTVVT LLVPEAERDK ANGLVGAVQC VGFLVTSVIA GSAIGFLGME ITLWICLGLS
 LVALLHLLPI RVDEPEIITQ EDAQPTVSDD SVPTPTSLLA IVSKGIDLKGM SKMKILSVPG
 LLALVLFASF NNLIGGVYSA LMDPYGLELF SPQLWGILLG LTLSGFIVGG AVISKTKGLCK
 NPVRTLLLVN VGVAVFGMLF AIREWWWLYI LGIFIMFAT PAEEAAEQTI LQRVVPFRQF
 GRVFLGMAV EMAANPLSTV IVALIAEAYL IPWMAGPGAD TIWGVILGEG KARGMALMFL
 ASGATMLVVV LLAFMSRSYR KLSQYYATTS QDIAGAAEK

> RXA01674 (1-894, translated) 298 residues
 MONGWNLQT LALFVAIVVEE GSLGAGARKV GMAQPNASRA IAELEADMKA ELLVRHPRGS
 HPTAAGLALV EHSRDLQSV QEFTEWVTEG RTEQPLKLHV GASMTIAEAL LPAWVADMRT
 RFPACRVDSV MNSSQVIEA VQKGLQLQF IETPHVPVRL HARVQEDKL IVVISPNHEW
 ANRTGRISLR ELSETPLIVR EVGSGTREAL QELLADYDMA EPIQVLNSNA AVRVVVEAGA
 GPAVLGELAL RDHALGRLLL SVPFEGSGVT RFLTAVWNSGP RRLPILAGEL VSIASNNHI

> RXA01873 (1-1092, translated) 364 residues

MSQAIDSKVE AHEGHEGHEG IERGTRNYKR AVFAMLAAGL AAFNGLYCTQ ALLPTMTEEL
GTPPTESALT VSATTGMLAL CIVPASILSE KFGRGRLVLT SLTLAIIVGL ILPLVFNITA
LILLRGLQGA LLAGTPAVAM TWLSEETHPK DIGHAMGIYI AGNTVGGLTG RMIPLAGLLEV
THWQALLGS STAALEFVVI MVVLLPKQRK FQPKNNINLRH EISAMAAHWR NPRLALLFPT
AFLGSGTFFVS LNNYLGFRMI DQFGLSEVLV GAVFIMYLAG TWSSTQAGAL REKINGSGTV
IFLSLTMIAS MALMGINNLM VTLVALFVET AAFALHSSA SGWIGIIATK DRAEASSMYL
FCEY

> RXA01917 (1-201, translated) 67 residues
MAQGTVKWFN GEKGFGFIAP NDGSDALFVH YSEIQSGSFR NLEENQPVFV EVGEGAKGPQ
AQQVRAL

> RXA01922 (1-1107, translated) 369 residues
LLFTAGWAAN HFASVVLVLR EQLDVSSVLV NGAFGIYALG LLPSLLAGGV LADRFGARMV
VLTPGGVLSAL GMLSLLAFFHD GPSLLVGRFI VGLGVGLVVS AGTAWAGRLR GASGVTLAGI
ILTAGFMMGP IVTSGGLMAS TSIITPFATIS VALSLIAVVV GFALGDARST PSALGASSGI
KHERSMKKAL AVSLPMAIIV FSCITTSILV MSARIDSTFG NAILLPGIGA AIAFASGLIA
QFLGRKFPAWG RGSIGVIGALC ALAGFALAAF GGDSIPVWL FVIASILFPTA YGLCLREGLL
SIETTYPLNR RGTGIGIYV FTYLGFGLFV LLDALLPHLG ASIPLYALAA LALGSAVIRG
VQIKRGYV

> RXA01936 (1-822, translated) 274 residues
MLLMQTGAIV GPLIAGALIP LIGFGWLYFL DVVSIPTLW AVWSLPSIKP SGKVMKAGFA
SVVDDGLKYLA GQPVLLMVMV LDLIAMIFGM PRALYPEIAE VNFGGGDAGA TMLAFMYSSM
AVGAVLGGVL SGWVARISRQ GVAVYWCIIA WGAAVAALGGV AIVVSPGAVT AWAMFMIIM
VIGGMADMFS SAVRNAILQQ SAAEHVQGR QGVWIIIVVG GPRLADVLHG WAAEPLGAGW
TVLWGGVAVV LITAIICMVAV PKFWKYEPK ITGI

> RXA01937 (1-426, translated) 142 residues
VSFRDIFADT RPLKEPAFKR LMLGNVATVI GAQLTVVAVP VQIYQMTGSS GYVGLTGLFG
LIPLVIFGLY GSGIADAFDK RIVLICITTI MCVTTAGFWV LTLIGNENIW LLINFISLQQ
AFFAVNQPTR TAILRSILPI DQ

> RXA01984 (1-279, translated) 93 residues
MHESGKNPKV VVDSQAPQGR GGHGGHIKR RPIPRQTEIS EVRRYIVMTA LALGGFAIGV
TEFVSMGLLS AIASDFEISE DQAGHIITIIY ALA

> RXA02060 (1-339, translated) 113 residues
EFARILPKPG QVIVLTADTG HLAELREPLG IIDVEAGKVD RMIEQAAGHL KPVGERDLVE
FEMLLDQKSI ASQIGMSFSA RHIKPEALAE RIAALPEQMK VTARAKITRL ERI

> RXA02087 (1-1347, translated) 449 residues
MTPIVESRAW KALGALSVEL FLTLDDQSLV AVALPKIQED LGASLNQAVW VSAVYLLTFA
VPLLTIGRLG DRYGQRNIYL AGMAVFTLAA LACVFAPSE WLIAARAVQG LGGSLNPPQ
LSIIHKIFAH DRRGATGVW SAVASSAGLF GPVIGGVVLG WISWRAVFLV YVPLGLISLF
MVARYVPKLP TGTSKIDWLS GAVSLVAVLG VVLAQQQPE LGWGTLIWVS LAVGIAAAVL
FIWMQTRSKA PLMPRIKFTK RNFAIGAFESI FSLGFTVYSV NLPIMLYLQT AQGSSSQLAG
LMLVPMGIIS VVMSPVIGRL VDR LAPGMIS KIGFGALIFS MALMAVEMTA NLSFWLLIP
IILFGSSNAM SFAPNSVIAL RDVPQDLVGS ASGFYNTSRQ VGAVLGAATL GAVMGIVGVT
VSFGVAMGAA IILTVLPLIF GLAVTQFR

> RXA02088 (1-1215, translated) 405 residues
MLPKIELEA KPKIPEEIVV LVVAAFIIL GYGLIAPIL QFVGVFDVSF AAASAVVSIF
AGARLLFAPM SGSLIDKIGS RRVYLTGLLT VAITTGLVAL AQEYQWILL RGTAGIGSTM
FTVSAMGLIV KMAPVEIRGR CSSVYASSFL FGNIIIGPVVG AAMSGLGMWR PFAIYGASVG
LAALVWVRM PKNDSLRKA DSNVSPALRF AEAIKDSAYR SALFSAFANG WSFNGVRVAV
LPLFAAAAFS NGGAIAGFAM AFAAAGNALC LQFAGDLSDR IGRKPMIISG LIVNAVFTAM
IFGTEVWIL ITVSALAGAG AGLLNPSQQA VLADVIDSRP GGVLANFQM AQDFGAIVGP
ILVGMIAEQA GFQIGFMELG VISLLAAVAV IFGRETLPTA KVEQV

> RXA02116 (1-906, translated) 302 residues

VSVAAEKGKLF TPTFVMGWFA NLFQFLVFYF LITTMALYAI KEFQASEVEA GFASSSIVIG
AVFSRFFSGY IIDRFGRRKI VLIISVLVTTI ACALYLPIS LPLLYANRFL HGVGYAFAAT
AIMAMVQELI PASRRSEGTG YIALGTTVSA ALGPALALEV LGTFDYDMLF INVLTATSVIS
LIAVVMYFK TSDPESGEP AKFSFKSIMN PKIIPIGIFI LLICFAYSGV IYAINAFEE
RLITGAGLF FIAYAVSMFV MRSFLGKLQD RRGDNVVIYF GLFFVVISLT ILSFATSNWH
VV

> RXA02159 (1-513, translated) 171 residues
MSLGSTPSTP ENLNPVTRTA RQALILQLID KQKVTQVQL SELLLDEGID ITQATLSRDL
DELGARKVRP DGGRAYAVG PVDSIAREDL RGPSEKLRRM LDELLVSTDH SGNIAMLRTP
PGAAQYLASF IDRVGLKEVV GTIAGDDTVF VLARDPLTCK ELGELLSGR T

> RXA02184 (1-381, translated) 127 residues
VPVGTVMKVV AERGFGEVSN PGGEDCFVGK QVLEKGVTEL HKGQRIDDFD AAGRKGQPAL
RKILETPRR RPQHKYKPEE LNGMISDLIT LLESGVQPG L AKGQYPEHKA GAQVAEILRV
VAKELES

> RXA02200 (1-1110, translated) 370 residues
MTNSTQTRAK PARISFLDKY IPLWILLAMA FGLFLGRSVS GLSGFLGAM VGGISLPAL
GLLVMMYPL AKVRYDKTKQ IATDKHLMGV SLILNVVVG ALMFALAWLF LPDQPELRTG
LIIVGLARCI AMVLVWSDMS CGDREATAVL VAINSVFQVA MFGALGWFLY QVLPSPWGLP
TTTQFSFWS IVTSVLVFLG IPLLAVFSR IIEGKIKGRE WYEQKFLPAI SPFALIGLLY
TIVLFLSLQG DQIVSQPWAY VRLAIPLVYI FVGMFFISLI ASKLSGMNYA KSASVSFTAA
GNFELAIIV SIGTFGATSA QAMAGTIGPL IEIPVLVGLV YAMLLWGPKL FPNPDTLPSS
ARSTSQIINS

> RXA02201 (1-363, translated) 121 residues
MAAALAKKHA GDALKVYSAG TKPGTKLNQQ SLDSIAEVGA DMSQGFPGKI DQELIKRVDR
VVILGAEACL EMPIDANGIL QRWVTEPSE RGIEGMRMR LVRRDDIDARV QNLVLAELTQN
A

> RXA02202 (1-639, translated) 213 residues
MTGQAAPNLH TNILNRIANE LALTYQGVFS AETINRYIFE SYVSLARTAK IHTHLPILAE
GFAKDRHLAL AVAEGKVASP VPQVLFICVH NAGRSQIASA LLSHYAGSSV EVRSAGSLPA
SEIHPLVLEI LSERGVNISD AEPKPLTDDV IRASDYVITM CGCDVCPMPY GKHYLDWELA
DPSDEGEDKI QEIIIEIDGR IRELWKSIDL SQN

> RXA02205 (1-879, translated) 293 residues
VNEEITLLAA AADPAATENI GWVQTIIVLSI VQGLTEFLPI SSSGHLRIIS ELFWGADAGA
SFTAVVQLGT EAAVLVFFAK EIWQIITGWF AGVFNKERRG FEYRMGMWII VATIPVILG
VLGKDLIREA LRNMVITASV LILFSLVFIL AERMGKKERD YDKLTMDAFI IMGLAQCLAL
IPGVSRSGGT ISAGFLGLK REVATKFSFL LAIPAVLGSF LYSPLPKDAF SSQGAASGLQ
LTVGTLVAFV VGYISIAWLM KPVANHSFSW FAAYRIPAGL LVMLLLALGM LNP

> RXA02273 (1-945, translated) 315 residues
MSYTSFKDD KALIGIVLSV LTFWLFAOST LNIGPDMATD LGMSDGTMMI AVVAAALFCG
TFIVAAGGIA DVFGRVRIMM IGNILNIGS LLIATATTS L ATQMVTIGRV LQGLAAAAM
SASLALVKTY WLGTDRQRAV SIWSIGSWG G TGFCALFAGL VVASPFGRWG IFALCAVSI
VAIALTRHIP ESRPAQSIGM HLDWSGIIVL ALSVLSLEF ITQGESLWGT HWMWTLLAV
SLTFLAVFVF IERIASWFLV DENLFKDHAF SGATITNFM I SATGGVVAVV MWVQGMWGV
SPTISGLTSI GFAAF

> RXA02282 (1-336, translated) 112 residues
MQESSRDNFQ VDLGGVVDLL SRHIYSGPRV YVRELQNAV DACTARSEQG EGYEYSIRI
RPVTKDRATF SLVDNLTGLT AQEARELLAT VGRTSKRDEF GLQREGRLQG FG

> RXA02305 (1-952, translated) 284 residues
MPAFEAMPGM PYWIDLSTSD IAKSAHFYEN VLGWEIEEYN DGYRMARLQG LPVAGLIDQR
GESSIPDTWI TYFLSYDLDA TAKKIAELGG RILAEPDTH LGRMILAVDI AGALFGVIEP
GSEESFVAAQ EPGTSVWHEL TTVSKYSEAI DFYGELEPTW TSEMASAEDD SFRYTTLALAD
GSFAFAGIDA KGHFFPPQVS FWQSYLGLVN ADDAAAKAKE EGGDVIRKPW DSFEGRMVLI

006603208.062300

SDSTGATITL CEVEEYVEEA AEGDDLFDID LSAFEEQFRK QEGQ

> RXA02431 (1-1191, translated) 397 residues

VVVTPRHIVY SAASRRVFI VEKRAIVER LSIDEGFMEP EALVGATPEE VKQWAEELRA
 EIKEVTGLVPS SVGAGSGKQI AKIGSGEAKP DGVFVVPVDK QHDLDDLPLV GALWGVGPVT
 GSKLASMGVE TIGDLAALTQ KEVEISLGAT IGISLWNLAR GIDDRVPEPR AEAKQISQEH
 TYEKDLLTRQ QVDAAIRSA EGARHRLKLD GRGARTVSVK LRMADFRIES RSYTLSYATD
 DYATLEATAF RLARYPGEVG PIRLVGVSFS GLEESRQDIL FPELDQIIIV PPAPDQYEV
 GVQSSSSSES TQVEAPQDVA LSMWCATQDV YHPEYHGWV QGAGHGVVSV RFETRSTTKG
 RTKFSMDDP DLTPADPLDS LDWADWFAEN GETGDDE

> RXA02446 (1-435, translated) 145 residues

MAIESIAYTS EALSTGSGRL GHRSTDGAL EFEMTPPKAL GSGEGTNP EQLFAVGYYAC
 FHSAMHSVAR SRKITLEDTA VGARVSIGPN GAGGFETIAVE LEVSIPLQLP AEAQELADAA
 HQVCPSYNTA RGNISVTVSV IDEEA

> RXA02541 (1-1185, translated) 395 residues

VNNSEWANKN YYADLGVSSS ASEDEIKKAY RKLARENHPD KNPGDKAAED RFKKAEEAYD
 VLGGDKKKRKE YDELKALLAS GGIRGGFGSG GAGFPGGFRT STGGFDTSDL FGGGQGGGFS
 TDGGLGDLFG GLFNRGAGSH QSARPTRGAD VQTEITLSFV EAAKGTTIPV ELTGDAPCNT
 CHGSGSGSGH PAKCGTCDGT GFTSENKGAF GFSAPCATCG GTGEIITDPC DNCHGRGTVR
 KSRSTIVRIP TVGEDGQKVR LAGQGEAGPN GKPAAGDLFVK VHVKKDDVFT RDGSNILITI
 PVSFSEALALG GAISVPTLNK PVKCLKPAGT PDGRTLVRVG RGIEARDSTG DLLVTVQVSV
 PKNLDDNAE ALRAYAEAE NSGDFPRANW AGQNR

> RXA02542 (1-654, translated) 218 residues

MTTPNGMPDN PGDPENTDPE ATSDRAEQA AEEAAARQAE ESPFGQASEE EISFELEAEI
 NDLLSDVDVP LGGDGEVSVA ETQLAERTD LQRVTAEYAN YRRATEREQ GIIDTARAGV
 VTQLPLDLDD LDLAQHGDL NEGPLKSLSD KLINILGGLK VESFGEIEA FDPETHEAVQ
 DLSQGDVKVL GTVLRKGYRL GDRVIRTAMV LIGDPEES

> RXA02543 (1-1854, translated) 618 residues

MGRAYGIDLG TTNSVSVLE GGEPPVIANA EGSRTTPSVV AFAKNQGEVLV GQSANKQAVT
 NVDRITIRSVK RHIGTDWSVA IDDKNYTSQE ISARTIMKLK RDAEAYLGED VDAVITVPA
 YFEDSQROAT KEAGQIAGLN VLRIVNEPTA AALAYGLEKG EQEQTILVFD LGGGTFDVSIL
 LEIGDGVVEV RATSGDNELG GDDWDQRIVD WLVEKFGQSSN GIDLTCKDMA LQRLAREAEK
 AKIELSSSSS ANINLPYITV DADKNPLFLD ETLSSRAEFQK ITQDLARTK TPNQVVFKA
 GVSVSEIDHV VLVGGSSTMP AVTELVKELT GGRPEPNKGVN PDEVVAVGAA LQAGVLRGVEV
 KDVLILLDTP LSLGIETKGG VMTKLIERNT TIPTKRSETF TTAEDNQPSV QIQVFGERE
 IATANKLLGS FELGGIAPAP RGVPQIEVTF DIDANGIVHV TAKDKGTQKE NITTIQDGS
 LSQDEIDRMI KDAEAHADED KKRREEQEVN NNAESLVYQT RKFVEENSEK VESDLKAKVE
 EAAKGVEEAL KGEDLEAIIKA AVEKLNTESQ EMGKXIEAD AXAGATQADA GAEGAADDNV
 VDAEVEVEDDA ADNGEDKK

> RXA02586 (1-270, translated) 90 residues

MHLLRDNNWV APGFVKKAYT VMHGSEVEE APRPTTTRLN DDEEVTVEHA VVAGDVTASR
 GGLSTQENRD LVSFVELKAR LEKRRLEDLD

> RXA02587 (1-2091, translated) 697 residues

VFSKNGHFAY RFRRIVPLVV IAAIALLFVI FGTKLGDGRMS QEGWDDPGSS STAAARIELE
 TFRGNDGDV VLLFTAPEGT SFDDAEVFSF ISGYLDGLIE NNPDEVSHIN SYFDTRNQNL
 LSKDGTQTFA ALGLKGDGEQ TLKDFRIED QLHPDNLAG VTEVAGATA VADALDEGMA
 GDLSAEVFA LPFVAILLLI VFGSVVAAAM PLIVGILSLG GLSLAILAIA GFFQVNVFAQ
 SVVTLGLGLL AIDYGLFMVS RFREEMDKGT PVEQAVATT ATAGTKVVFS AAMVAVALSG
 LVFPFOAFLK SVAFGAISAV GLAALMSVT LPSLFSMLKG NIDKWSLRRT ARTARLEDT
 IWRYVPANAM RHAKAVTVGV VLLLLLALTVP LTGVKFGGIN ETYLPPEAND RVAQERFDEA
 PPAFRTPEVK LVVTGADNNQ LIDIYQANE VEGLTDRFTA GATTDGTTV LSTGIQDRSL
 NEQVVEQLRA ISVPEGVEVQ IGGTPAMEIE SIEALFEKLL MMALYIVLAT FILMALVFGS
 VILPAKAIIM TILGMGATLG ILTLMFVDGV GASALNFSPG PLMSPLVLVI MAIYGLSTD
 YEYFVLSRMV EARDKGESTD DAIRYGTANT GSIIITAAALI MIVVCGAFGF SEIVMMKYIA
 FGMIAALILD ATIIIRMLVVP RRDAPASRRQ LVGTRRL

> RXA02861 (1-1083, translated) 361 residues
 MSTRTPQDR TYDEYGIERV NKDEPLVDK LRDKHDFWDH LMRMRNERFGA KGGNQLSAGI
 TYFSVLSIFP IAMLVFGIAG VILAGNEPVL TDIQNRINDA LEIGEIGNTVN GIIDSIAIQR
 GAVLIGGGVT ALWSGLGWMA NLRFGVSRMW AIDPTEGNFI QKKLTDLVAL IVLLLAMGVA
 FGITLALGAS LTKNLLDFVG LGEIPGISYI TWVVAALGVV LANFLVFMWL IFSLPRTKVP
 MKPGLQAALL GAIGFEVVKQ VGSLLASNAL SNPAGAAFGP IIGIMVVLVL IWRLIMYCSA
 WAATSEEARL LATVPAPERA IIRVRHEIDF GEEVSQSARK VGIGVAVGAA TAGAFALLRK
 K

> RXA02878 (1-357, translated) 119 residues
 CLSTVDEFAF CWSSFADTSW FSSALALLFT PLMTVALASV PDNMYGHGSA ILNTLQQLAG
 AAGTAVMIATV YTSVSNNALI DGATQQTALA DGANSAFFAS ACVAVFALIV GFVFKRPAR

> RXA02893 (1-606, translated) 202 residues
 LVLAFVLVLL VFRSIWVPLI AALGFGLSVL ATFGATVAIF QEGAFGIIDD PQPLLSFLPI
 MLIGLVFGLA MDYQIFLVTR MREGFTKGKT AGNATSNFGK HGARVVATAA LIMVSVFAAF
 IAQDMAFIKT MGFALAVAVF FDAFVVRMMI IPATMFLDD KAWWLPKWLD KILPNVDVEG
 EGLSELHEAR TEELKENVGV GA

> RXA02907 (1-726, translated) 242 residues
 VAKFLYKLGs TAYQKWPPFL AVWLIVILIGI TTAGLYAKP TSSSFISIGL DSVTMEKMQ
 ERFPSDDAT PAFTSGSVVIQ APEGKILTDP EVGAENVQML DEVRATGVLK DADSVDPVL
 AAQGVAQMT SABLEAQGVA EKIAADIESI SPLSADETTG IISMTFDADS AMDISAEDRE
 KVTNILDYED DGDLTVVYNG NVFGAAATSL DMTSELIGLL VAAVVLIVTF GSFAAGMPL
 IS

>RXN00034 TRANSLATE of: rxn00034.seq check: 3201 from: 1 to: 1449
 MSYTSFKGDDKALIGIVLSVLTFWLFAQSTLNI GPDMDTLGMSDGTMMNIAVVAALFCG
 FTIVAAGGIADVFGRVIRMMIGNILNIGLSLLIATATTSLATQMVITGRVLQGLAAAAIM
 SASLALVKTWVLGTDRQRAVSIWSIGSWGTFGCALFAGLVVASPFQWRGIFALCAIVSI
 VAIALTRHIESRPAQSIGMHLDSWGIIIVLALSLSLELFIQTQGESLGWTHWMTWLLAV
 SLTFLAVFVFIERIASWVDFNLFKDHAFSGATITNFMSATGGVVAVVMVMQMGV
 SPITISGLTSIGFAAFVILFIRVGEKAMQKVGARAVIITAGILVATATALLMITAVSESTY
 IVISLAGFSYLGGLGFATPVTDALGTLPKDRTGAGAGVEKMSLSLGAALGIAISTSV
 FLALRDGTSINSDELALAGTVSLGINVVFAATATITAAVLIPKAAGKVSQTSITLPEPAIA
 VKI

>RXN00046 TRANSLATE of: rxn00046.seq check: 4489 from: 1 to: 696
 MDLNTGRSKLYAQLQGQLIVSVQAPDGHAMRDTHTLTHVAAACVDGGAPAIRCGGYGGLLE
 DIRSINRVDVPVFGTLTKEGSEGVYITPTRDSVRAVAESGATVVCADATFRPRPDGSTFA
 ELVTVAHDSGILIMADCATPEEVLSAHKAGADFVSTTLAGYTEHREKTVGPDFCLREAR
 ELVPDAFLIGEGRSNPADVAHGRGLIGANAIIVGTATIDPGFITQGFASLLH

>RXN00165 TRANSLATE of: rxn00165.seq check: 9424 from: 1 to: 1416
 VASAGMAASFCNGLTPIVIGKAVDEAIGTSDLQRLWFMIAMLAFLTAMTVNNIARYM
 LVRSQQLVSHDLRLMLVDRIQDPRGFAGKERTAGGLLSIASSDTQRVGDIVMMTVFPVAE
 LASIYGAIVVMYSINPWLVAVLIGGFLVVVAIVQVSKPLQKRSGARQQAVAQAATATD
 VVOGLRLIKGLGAIIVTRRRYEAISSGEAYRKTVHADAAEARLNGVTDAAGAI FVSALGIG
 AGFLALQQMSIGDLITVVGLTQFLIMPMTMLGRNVASRWASAEASAKRIRGVLGADFER
 VSAHADAKAEIEITQQLAKGLTVIRGTDEQLVEVLEQLPRTRIVAPHAADLPQSGRVN
 HPVAEVAEKAEIVASCDITPGSSKIVGEGRLLSGGQRQVALARAIFDPPEVLVLQDP
 TTAVDVSVEQNIAQQVAAHRAGKVTIVFSEAPAWSAVADQHVAAALREVVMK

>RXN00380 TRANSLATE of: rxn00380.seq check: 9027 from: 1 to: 621
 VRLTKLAATIGCVTLISGLALVACSSDSTAGTDAVAVGGTFQFHS PDGKMEIFYDEADRQQ
 LPDIGGDSLMEEGTQINLSDFENGVVILNAGQWCAPCRSESDDLQIIHEELQAAGNGDT
 PGGTVLGINVRDYSRDIAQDFVTDNGLDVPYSIYDPPFMTAAASLGGVPASVITPTTVLQDK
 HRPAAVFLREVTSKDVLDVALPLVDEA

>RXN00453 TRANSLATE of: rxn00453.seq check: 3260 from: 1 to: 2349

VISAWLLILAI VGGALTMQKGFNSFTTIEDTPSIDATVSLVENFPDQTNPVTAAGVNVV
 FQSPQETTLDDQMMTAMDADVVDYIEDNLDPFGGGERFGNPVEVSPALEEMVIEQMTSMG
 LPEETAAKDAANLAVLSEDKTIGYTSFNIDVEAAEYVEQKHDRVINEAMQIGEDLGRVRE
 AGGPAFGDPTQIETTSEIIGIGIAFVILITFTGSLIAAGLPLITAVIGVGIGALAIVLAT
 AFTDLNNVTPLVAVMIGLAVGIDYALFILSRYRAEYKMRPRADAAGMAVGTAGSVAVFAG
 ATVIIALVALIADIGFLTAMGISAAFTVFVAVLIALTFIPALLGVFGGHAFKGIKPGIG
 GNFTPKQTWEQALNRRSKGRSWSVKLVQKAPGLVAVVVLGLGALTIPAMNLQLSLPDSST
 SNIDTQQRQADLMAEGFGAGVNAFPLVIVDTHEVNADSTALQPLIEAQEPGEGEFDREQ
 AARFATYMYVTQTYSNIDVKNQIITSVNDFTAAQILVTPYTGFPADKETPELMHVLRAQ
 EAQIEDVTGTGLTGTGTAQVLDITTEQLEDAMPVYLAUVVGLAIFLLILVFRSLVLPLVA
 GLGFLLSVGAAGFATVLVWQEGFGGFVNTPGPLISFMPILFIVTFLGLAMDYQVFLVTRM
 REHYTHHNGKGPQSKYTPVEQSVIEBFTQGSRVVTAALIMIAVFVAFIDQPLFFTKIF
 GFALGAGVFFDAFFIRMGLVPASMFMLMGKATWMPKWLDRILPSLDIEGTALEKEWEEKQ
 AAR

>RXN00493 TRANSLATE of: rxn00493.seq check: 4601 from: 1 to: 1614
 MAKLIAFDQDAREGILRGVDALANAVKVTGPRGRNVVLDKAFGGPLVTDGVTIARDID
 LEDPFENLGAQLVKVSAVKNTNDIAGDGTATTLLAQALIAEGLRNVAAGANPEMLNKGIS
 AAAEKLLEELKARATEVSDTKEIANVATVSSRDEVVGEIVAAAMEKVKGKGVVTVESQS
 IETALEVTEGISFQDGYLSPYFINDNDTQOAVLONPAVLVLRNKISSLPDFLPLEKVVE
 SNRPLLIADVEDGEPLQTLVNVNIRKTIKVVAVKSPYFGDRRKAFFMDLLAIVTKATVVD
 PEVGININEAGEFEVFGTARRITVSKDETIIVDGAGSAEDVEARQQIRREIANTDSTWDR
 EKAERLAKLSGGIAVIRVGAATETEVNDRLKRVEDAINAARAAQEGVITAGGSGALVQI
 AETLKAYAEFEFGDQKVGVRALATALGKPAKYIASNAGLDGGSVVVTAALPNGEFNA
 TLEYGNLNDGVIDPVKVTSAVNVNATSVARMVLTTESASVVEKPAEEAADAHAGHHH

>RXN00535 TRANSLATE of: rxn00535.seq check: 586 from: 1 to: 717
 MWAGMSTAMLAYFLQTVAGLFGFTLLVQPVVLVLSIMFTLPLSARFNGYRLRTEIFWAT
 LITVAVGIMIVLGRPLPGNHPPLDRWIPVLLVGVAVMGGMWLLAEYVLKKDKALILGLV
 TGALPGYVAVMSKAAVDLFVHQGITGLIINWEGYGLITALLGTIVQYYSFNAGELQKSL
 PAMTIAEPIVAFSLGYLVLEKQFQVVDWEWIAMGIALLVIMVSTIALSRSTMPAGSKR

>RXN00575 TRANSLATE of: rxn00575.seq check: 5920 from: 1 to: 537
 MVERDFTIRPIREGDFPQVRDIYELGETGHATYETSGPTWDQFQSKIMDTVMVAVERN
 DPDFILGNVSAAPISSRQVVFHGVVEDSIYIHPQGGGRIGGALLDALITYCESNGIWSIH
 SWIFPENLGSAKLHESKGFFVKVGTMHQMARMPYGEQWQRDCDLWECLLSVPEQAQSS

>RXN00786 TRANSLATE of: rxn00786.seq check: 1529 from: 1 to: 975
 MSSPVISPEPTKGGKILLAAPRGYVAGVDRAVETVERALEEYGAPIYVRKEIVHNRVVD
 TLAEGKATFYNEASEAPEGANMVSFAHGVS PMVHEEAAKNKIKADACPLNIVKHKEVQ
 RFDKQGFHILFIGHEGHEVEGTMGHSVEKTHLVGDVAGIATLPEFLNDEPNLWLSQTT
 LSVDETMEIVRELKVKFPLQDPPSDDICYATQNRQVAVKAIARCELMIVVGSRNSNS
 VRLVEVAKQNGADNAYLVDAIREDPAWFGEVETIGISSGASVPEILVQGVIERLAEPGY
 DVEEVTSAEAKVIFVALPRVLRHN

>RXN00788 TRANSLATE of: rxn00788.seq check: 4194 from: 1 to: 225
 MASSINIGVFNLGNVAAWLAGATITTSGLTISAGLVGLMSTLSGLVLAIIVAVLRRKAQ
 GTQATISVVEHQPAQ

>RXN00803 TRANSLATE of: rxn00803.seq check: 768 from: 1 to: 1230
 MGVSALNMSDMVANKRAQRKVMALVALSVFTVWAGGNETPLLVFVYRGEFFSNLFIIDLL
 LVFYAIGVAVGLLAAGPLSDRYGRRAVMLPAPLIAILGSAIASGEETAILIAIGRVLSG
 ISVGMVMTAGGSWIKELSSSRFEPGVKTSAGAKRASMSLTGGFALGPALAGVMAQWLPPLP
 GQLAVVLHIILTLILFPLLIATAPETRQSAHLKTKGSFWSVDVLPVPSALDKRFLFVVAFTGP
 WVFGAFTAYAVLPSQLRDMVSAPVAYSALIALVLTGSGFGFIQGGPQIMGTSKTRGPIL

AMFVTVIGMIGAVIVVMNPHPWALVGCMLGLSYGLCMFMGLAETQNIAPPDIMAGLTG
IFYCLTYVGMVFPALMTWLNQWLSYFPMGLGFAVMATICLIIVFSFARRE

>RXN00829 TRANSLATE of: rxn00829.seq check: 7202 from: 1 to: 2340
MQKADSHDWISVHGANNENLNKNSVRIKRRLTVFTVGSVSGKSSLVFGTIAAESRLIN
ETYSTVFQGFMPMSMARPDVDHLEGITTALIVDQEQMGNPRSTVGTATDATAMLRILFSR
IAEPNAGGPGAYSFNVPSVSASGAITVEKGGNTKREKATFKRTGGMCPACGCMGRASDID
LKELFDASLSLNDGALTIPGYTGGWSYRMYSESGLFDAAPKIDFTEEERHNFLEPT
KMKIAGINMTYEGLIPRIQKSMLSKDREGMQKHIRAFVDRVATFIPCPACGGTRLAPHAL
ESKINGKINIAELCAMEVRDLAKWIKTVEAPSVAPLLTALTETLONFVEIGLGYIQLDRPA
ETHSGGEAQRTKMIRHLGSALTDTVYVDFEPTAGLHAYDIERMNKLKLLDLRDKGNTVLVU
EHKPEITIAIDHVVLDLPGAGAGGGEIRFEGSVDKKDSDTVTGLHFNDRASLSKESVRAP
HGALEIRGADRNNLNNDVDIPLGVFTAISGVAGSGKSSLIHEIPRODESUVFVDQTAIGH
SNRSNPATYTGMLDSIRKAFKANDVKPALFSPNSEGACPNCKGAGSVYVDLGMMAGVSS
PCEVCEGKRDESVLDYHFGGKDIADVGLLSAANAYEFAAKDSKILPAAKAKRRLVDVG
GLYITLQGLPTTLSGGERQRLKLATHMADKATTFILDEPTTGLHLADVTLDDLDFQDLVD
DGKSVIVIEHHLGLVLAHADHIIDVGPAGSGDGSIVFEGSPAEILKTDPTTGRHLKAYVD

>RXN00833 TRANSLATE of: rxn00833.seq check: 7757 from: 1 to: 495
MAKTHFGGNETATSGELPQVGDNLAEFNLVNTLGEVSSKDFQGRKLVNLNIPFVDTGVC
ATSVKFNENAAASLENTTVLCISKDLPALGRFCSAEGIEINVTPVSAFRSTFGEDNGIVL
EGSPLKGLLARSVIVVDENGKVAYTQLVDEFTFEPDYDAALAGLN

>RXN00901 TRANSLATE of: rxn00901.seq check: 5066 from: 1 to: 414
MQKKQQLSTALIMGLALLSASSALATDMYLPAMFGIAEDLGTAPMVQLTLSSFMAGMAI
GQLIIGPLSDQLGRKGLLVAGAVAALVASVVCALAPSI SVLVIARLVQGLGGGACVVLRA
RSCQTLNADKRLRTPLHC

>RXN00932 TRANSLATE of: rxn00932.seq check: 6704 from: 1 to: 474
MTPQKLHRFAALLEMGTTWLLIIGMILKYSGVTDVATPIAGIHHGFGFLCFAAITITVWI
NNKWTTFPQGIAGLIVSVIPWAALPFALWADKKGLVAGGWRFSDFSEKPHTFDKILAQVL
RHPFIRSILILLVIIAVVPSILLAMGPPYDPDAIANTVD

>RXN00937 TRANSLATE of: rxn00937.seq check: 2481 from: 1 to: 372
MATIDVTEETFEFSTVTDGIVLVDWASWCGPCRQFAPTYEKKVSETHTDATFAKLDTEAN
QGLAAALQIQSPTLTMVFRDGMVYREAGTMPAPALDDLVNQVKALDMDDDVRQVAEQQG
SAEA

>RXN01010 TRANSLATE of: rxn01010.seq check: 367 from: 1 to: 1119
MKKLQMPAILVGGFVGPFTGQALSVDLPEFADTFDISVQAAALMTAYLLPFPATMMLFSG
RITRKIHHPKVQAAIYVTLPLALLLVTPSWGFLMAAYATIGIANAFITPVLQIMLREL
VPPRSLGKALGYAAMQSLGMLSAPLIAGVSSVSWRLTFLVTAASLFLVARLPVPP
PSASKQNVSGKVQWGPTIIMVSGFVVGIGIIGIGFMTSLHVGEQFGLDAAARGLVVMCG
GLAAFFASRKIGDLADKFGVRAVLIVSAVIGITIALALLPFIAPWIIVVAVLWAFVAAQAQ
IQATVNLAVIGSPGGSSLLSTVQAQFRFGSAAAPVTFELPIYMGIGSGAFVWSAVALFFVA
IAQWLNQPRVERG

>RXN01091 TRANSLATE of: rxn01091.seq check: 7053 from: 1 to: 564
MVPNTVLIDHETADLATQIRLEHIMACLRDPVSGCPWDIEQTFASIAPIHTIEEGYEVAD
AIAQEDWPELRGELGDLFQTVFHAQMAREAGHFALVDVVKASIDKMLRHPHFVGAQSN
AKSADQQVEDWEVIKAPERAGKQKGVLDGVALGLPALMRATKLQNNAAVRGVGDFWPDIGQ
VLGVKTEE

>RXN01102 TRANSLATE of: rxn01102.seq check: 7618 from: 1 to: 1245
VAVLVAVAAAFGWSLLLPVVLAVLNNGGSSAVAGATTGIFMAATVITQIFTPAALRKI
GYTPVMAFAAFMLGVPAIGYIFSVEPIPVLVVSLRIGIGFALTVAESALVAELVPVRFL

GKASGMLGVFIGLSQMLFLPAGLALGDQFGYNVYVVLGAVIALVAAMCLRIPQVKAAR
 QQPQVSEQRSSVSTWKLVLVPSLAVTSLSMTFGAVSSFLPAAVIELDPGLGAALAGIILS
 ITGGSSMVFRYLSGVIADRRGVPGTMTIPAQIIGFLGVVLTITVTIFQGWSVLLIIAGVM
 FGGAFGMVQNEALLSMFFRLPRTRVSEASATWNIAFDSGTGIGSFLGLGIVAAASLYASGAF
 GSGAVVILFGVILTTADRIIGHRRITEYNNTRARLRQVFVARRAVQGLRNRKDKR

>RXN01190 TRANSLATE of: rxn01190.seq check: 7061 from: 1 to: 1347
 MWQSEALVFPIAIGLIVDHAIVTKDLRLVVLGVAFVVLVVLFSNRFSGSRLNRAVNF
 ESHALRVEVADHALKNLDPNRLVPGVEVMSRSTADADSSTRIFGQIGTGVSAAATGFLGAAT
 YLLTSDNLIGLLVLVLVPIISGVVALASKGISKRSVTQOEKLAESGAQASDIMMGLRVIK
 ATGGERWAVKTFEKASQASARAADTVASGKGVAGIGELSTAVNLAALLAGWRVTTTGE
 LGPQQLATIVGVAVYLSEPIRLLSNSINASIAHGAERAVANFLNLDSEQAQYESSSETIN
 DGEFLVIVPPASTLPHGDNILATPHAADIFEGLTRLSNISMNHEDNVPIDPQVIRASGLTD
 IIEVDGLDAPVRDTSNLSGGQQRQVALARALHADAELVLMDDTSAVDSVTEVSIAQGI
 KQLRAGKTTIVSSSPAFYNLADRVIISHV

>RXN01320 TRANSLATE of: rxn01320.seq check: 5093 from: 1 to: 1647
 MTSQVKKPDDERPVTTISKSGAPSAHTSAPYGAAATEEAEVEEKTGRGVFIIALMLAMLL
 SLSLQGTIFGSALEPTIVGELGGVNHMTWVITAFLLGQITSLPIFGKLGQDQGRKLYFMFAI
 ALFVVGSIIGALAQNMNTLIVARALQGIAGGGLMILSQAITADVTARERAKYMGIMGVS
 FGLSSILGPILLGWGTTDGPGRWRGLMLNVPIGIIALVAIVALLKLPARERKGVSVDMWLS
 IFMAIATTAFLAVFTWGGNEYEWASPMIIGLFTITLVAIVFEVEKRAVDPLVPMGLFS
 NRNFVLTAVAGIGVGGLFMGGTIAMPTYLQMVHGLNPTQAGLMLIPMMIGLIGTSTVVG
 IVSKTKGKYKMPYFPIGMLIMVLAIVLLSTLTPASALALIGLYFFVFGGLGCAMQILVLIV
 QNSFFITMVGSTATGSNNFFRQIGGAVGSALIGGLFISNLSDRFTENVPAAVAMSGEEGAQ
 YASAMDSFGASNLTPHIVESLPQALREAIQLSNDALTPIFLALTPIAVVAAILLFFIR
 EDHLKETHE

>RXN01345 TRANSLATE of: rxn01345.seq check: 9398 from: 1 to: 1452
 MRFGLDLGTTRTIAAAVRDRNGYPIVTVEDSLGDTHDEIPSVVALKADRIVAGWDAIEVGG
 DHPSEVRSFKRLLSEFPNVTEATPVYLGDHVHPLGAVLEAFENNVTLARAFQTLGDTSP
 IEVVIGVPANSHSAQRLLTMSAFSATGITVVLGVNEPSAAAFETHRHARTLNSKRQAI
 VYDLGGGTFDSSLRIDGTHHEVVSSIISIRLGGDDFDEILLQCALKAAAGRHDAFGRKA
 KNTLLDESRNAKEALVPQSRRLVLEIGDDDTITVPVNKFYEAAATPLVEKSLSIMEPLIGVD
 DLKSDSDIAGTYLVGGGSSPLVSRLLRERFGRVRHRSPPFSGSTAVGLAIAADPSSGFHL
 RDRVARGIGVFRHDSGRAVSFDLIAPTDTSATVAKRCYKAVHNIWFRFVEYSTVSED
 GSPGDISILLSEIKIPFDSITVDVDATEISRFDGPEVEETITVNDNGVASISIKILGGVTV
 EHTI

>RXN01553 TRANSLATE of: rxn01553.seq check: 7694 from: 1 to: 1320
 MTVQEFDRATKPTPKPIVSWAFWDWGSASFNAVLTFTFISVYLTDSVGATLPEGSNATS
 LYSMAVAIAGVIVAVVAVPMGRRSDIKGTRRRSLRMWTLVTVFLMFCLEFTRKNTDPTFFW
 FGVAIMAIANITFEFAEVQYQAQLSQISTRENVRGVSFGWSMGYFGGIIVLLVCLGFPV
 AGDGGTRGFLNLPIDEGMNIRLVAVLAAVWFLVSAIPALLRVPEIEAQVAEDHPKGLIA
 AYKDLFGQIAELWQDRNSVYFLIAATVFRDGLAGVTFGAILAVSVYGLSAGDVLLFVG
 AANVVSALGALLGGFLDRVRGPKPIILISLAIMADAAILFFVEGPTNFWIFGLLILCAFV
 GPAQASRSYLTRLSFDQEGQLFGLYATTGRAVSWMVPSLFGVFVGLTGDDRTGILAI
 LILLFGVILLSMVKPPHKVK

>RXN01559 TRANSLATE of: rxn01559.seq check: 3150 from: 1 to: 1842
 VLIVVGVALVLLTGDRSATPKLIGIDLQGGTRVTLVPGQDPTQDLNQARTILNERNVG
 MGVSASVADGNTLVITVPGENTAQAQSLGQTSQLLFRFVGQAGMPDMTTLMPLELEMA
 NRWVEYGVITEEQANASLEEMNTAVASTAVEGEATEPEPVTVSATPMDEPANSIEATQ
 RRQETIDMLRTDRQSTDPTVQIAASSLMQCTTDEMDFLAGTDPRPLVACDPAVGGVYV
 LDPAPELLNGETDEENGARLTGNEIDTNRPIITGGFNAQSGQMEISFAFKSGDGEESGALS
 SLTSQYLQQQIATLDSQVISAPOVQISATPVGSAISITGDTQTAEQDLANNLRVGALEL
 SFAGENGERRGTTTVPVPSLGAASLKAGLIAGIVGIALVAIVFAYYRVFVGSFLTFLFA
 AGVLYVGLLVLLGRWIGYSYSLDLAIGLIIIGITGTTADSFVVFYERIKDEIREGRSFRSAV

PRAWESAKRTIVTGNMVTLLGAIVIYLLAVGEVKGFAFTLGLTIVFDLVVTFITAPLVI
LASRNPFFAKSSVNGMGRVMKLVERRANGELDEPEYLKKIHAKNAAADKASTDNSSTDN
SEAPGTDTNQEEKK

>RXN01605 TRANSLATE of: rxn01605.seq check: 6399 from: 1 to: 1515
VTSDSPAPATVNAVFNNSNGFIASMLGNQVNVTVETMDTEFGVRIVDNMLVGSTLGDG
MNQAAEGATTLLSDGVGSANDGAVQLADGAVTLRDGIASANEGAQSLADGASQDITGLGSA
ATGCSQTADGLSSLSAGTAQLQGQATQVSDGVGQVLVDQVAPLTAIYVPDINSQITLDRDGA
ATIASELSDFPSTYRSYGVDSAVSASQQLAAGLQTLKDGSSQLSIGARTLADGTSQLAAGS
EQLVVQAQALRDGTQVLDEGSSSELALKLTDGASQVPTFADGADTTIATPVETEQAQDTP
LFGTGLAPFFMAVGLFMGATVAMMILHPISTRALDSRMGGFRGTASYPSTVLGLQCAT
IMNAVLYFLDLNPAHPAGLWAMVAISWVFSITHTMFNNVAGPSAGRVLSVMMSSQLV
SSGGLYPETQPAFFHWEHTYDPITYAVNLVRQMINETPSNDPRFIQAIWVLLFIWALM
LAISTLANRTNKVLRMKDYHPELKV

>RXN01676 TRANSLATE of: rxn01676.seq check: 7951 from: 1 to: 756
MILHGVVYAGLLVLLVPLGLGAGILGELFITQRQTIIVVSSIVLIILGFVQIFGGGDFD
MLHGLDLDRQSKATVTSGLGKSFLLGMTSSIAGFCSGPILGAVTLTAATSGNSISALI
LSAYGAGMVLPLMAIALWAKLGQRGQQLRGREFTFLGRQWHIVSVISGALI IAVGILF
WSTNGLVSMPELVPMDTQIWLQEATFSLGSLPLFDIALIIVAAAGFLYFWNKQRKRKEEAQ
RPKESGVWINPR

>RXN01837 TRANSLATE of: rxn01837.seq check: 8888 from: 1 to: 777
VSTNKERRQQALSQLEKEIKSRDRKEKTKPLTVVFFASLAVILVVVGGIYAATRSTEDV
ITADETSTAETPDYQPLALTRTALGDSVTCEYPDAGEASKOVSKPATENVFATGTVTV
NLTTAQAGNIGMELDRSVSPCTVNAVEHMASSEGYNDYVCHRTTSGIYVLQCGDPSSTGA
GGPGFSFANEYPTDEATDLTPVIYERGTIAMANAGADNGLPVLPLQLRGFTGTGLHLH
RDPHRRRRCPCNPRHRRSWH

>RXN01863 TRANSLATE of: rxn01863.seq check: 1675 from: 1 to: 1149
MNSVKLKQPVSIYNDPWESYNDVKEHGQTLTSLNIEFTTNLCNMRCSCHAVGYTLQTVDP
EPLDMDLIYRRLDEIPNLRMTSITGGEPMFSSKKSIRNVKPLKLYAHHRGIYTMQNSNLT
LQDDRYDIAEYIDVMHISHNWGTTDEFANVGFSGAMKQKPLKAKLKYEQMISNARTK
EQGMFVASAETMLNQSTLPLHRLKIHQEVVHDMKCSRHEIHPMPADFASQNLVLTAEKK
TIHIDLDFRDEIDWMLFGTLVPVFCCLKDDEQKLRLSLRNANNVTRNDPDGRSRLNVN
FTGNVIVTDFGDEGTISNIQKDKLTDVFDKWLSSDLAKSLNCHSEFSCPLGNVLYKNM
YYPNMDPKDNERRMHKQPIIQF

>RXN01873 TRANSLATE of: rxn01873.seq check: 8968 from: 1 to: 1236
MSQAIDSKVEAHGHEGHEGIERGTRNYKRAVFAMLAAGLAFAFNGLYCTQALLPMTTEL
GITPTEALTSVATTGMALCTVPASILSEKFGGRVLTISLTALIVGLILPLVPNITA
LILLRGLQALLAGTPAVAMTWLSEEIHPKDIGHAMGIYIAGNTVGGLTGRMI PAGLLEV
THWQNALLGSSIAALI FGVIMVLLPKQRKFQPKNINLRHEISAMAHRNPRALALFGT
AFLMGTFVSVLYNLGFRMIDQFGLSEVLVGAVFIMYLAGTWSSTQAGALREKINGSTV
IFLSLTMIASMLMGMINNLVLTVALVFVTAFAFFALHSSASGWIGIATKDRAEASSMYL
FCYYVGSSVIGWVSGFAFTHLPWLAFIGWLILLCGVLAIACVTLARLARNAN

>RXN01922 TRANSLATE of: rxn01922.seq check: 3553 from: 1 to: 1152
MRSGNANRVIGVTILLFTAGWAANHFASVLVLIREQLDVSSVLVNGAFGIYALGLLPSL
LAGGVADRFAGARMVVLTCGVLSALGNLSLAFHDGSPSLLVGRFTVGLGVGLVVSAGTAW
AGRLRAGSGVTLAGIILTAGFMMPPIVTSGLGMASTSIITPFAISVALSLIAVVVGFALG
DARSTPALSAGSSGKHERSMKKALAVSLPMAIIVVFSCTITSLIVMSARIDSTFGNAILL
PGICAAIYFAGLIAQFLGRKFAWGRGSGIVGALCALAGFALAAFGDSDIPVWLFVIASI
LFGTAYGLCLREGLLSIETYTPLNRRGTGIGIYYVFTYLGFGPLVLLDALLPHLGAISPL
YALAALALGSAVIRGVQIKRGYV

>RXN01926 TRANSLATE of: rxn01926.seq check: 2379 from: 1 to: 741
LRSFYTPEQAIEREGDVKAATEEAELLAADGAVHDQELFNCTTSPILFASAMLNFGVH
QILDTLQLLAPSAGRDADPKALEAATSAMDDHRDITDDFSGVVFVKVQAGMEKNHRDTLA

00603208.062300

FMRVVSGEFDRGMQVTHSQSGRSFSTKYALTVEGRTRSTVETAFFPGDIVGLVNAGALAPG
 LTI FEGKKI QYPPMPKFAPEHFRLRAKSLGKYQFRKALEQLDSEGVVQILKNLDRGDA
 NPGHGRC

>RXN01936 TRANSLATE of: rxn01936.seq check: 5923 from: 1 to: 1272
 VSRFDIFADTRPLKEPAFKRLNLGNVATVIGAQLTVVAVPQIYQMTGSSGYVGLTGLFG
 LPIFVIFGLYGGSIADAFDKRIVLICTTIGMCVTTAGFVWLTILGNENTWLLILNIFLQQ
 AFFAVNQPTRTAILRSILPIDQLASATSLNMLLQMTGAIVGFLIAGALIPLIGFGWLYFL
 DVVSIIPTLNAVWSLPSIKPSGKVMKAGFASVVDGKLYLAGQPVLLMVMVLDLIAMIFGM
 PRALYPEIAEVNFGGGDAGATMLAFMYSSMAVGAVLGGVLSGWVARI SRQGVAVYWCIIA
 WGAARVFGGVAVIVVSPGAVTAWAMFIMMVIGGMADMFSSAVRNAILQQSSAAEHVQGR
 QGVWIIIVVVGPRLADVLHGWAAPLGGAGWTVLWGGVAVVVLTAICMVAVPKFKWKYKPK
 ITGI

>RXN01984 TRANSLATE of: rxn01984.seq check: 3533 from: 1 to: 297
 MHESGKNPVKVVDSQAPQGRGGHIGGHIKRRP IPRQTEISEVRRYIVMTALALGGFAIGV
 TEFVSMGLLSAISDFEISEDQAGHIITTYALAWLVPR

>RXN02002 TRANSLATE of: rxn02002.seq check: 9539 from: 1 to: 378
 MGNANSDTAAEAHRRTFAVIAHPDAGKSTLTEALALHAHII SEAGATHGKAGRKATVS
 DMNMEKDRGISIASALQFEYAPEGHAGEPFMINLVDPGHADFSEDTYRVLMAVDAAV
 MLMHSV

>RXN02119 TRANSLATE of: rxn02119.seq check: 898 from: 1 to: 1641
 MTETLVVNLGAGYGHRTLFDNVNLTVAAAGDVVGVGVNGAGKSTFLKILAGVEKPLAGT
 IALSADAFVGYLPQEHTRTSGETIAVYIARRTGQCAATTAMDPTAEAFGADPDNAALAD
 AYAEALDRWMSGAADLDERIPVLADLGFELPTSTLMEGLSGGQAARVLAALLLSRFD
 IGVLEDPNTNLDLDGLEQLENFVQGLRGGVVLVSHDREFLSRCVTVLELDLHQNSHHYV
 GCGYDSYLEERAVLRQHARDQYEEFAEKKDLVARARTQREWSHGVNRNAIKRAPDNKL
 RKKAASSEKQAKQVQRMEGRARLEVEEPRKEKWLQFSVGKASRSSSVSTNDASFT
 TQGDFTLGPVSIQVNAIGDRIGITGPNAGKSTLLRGLGNQEPSTSGTATMGTSGVAIGED
 QARALLDPQLPLISAFEKHVPDLPISEVRTLAKFGLNDNHVERDVEKLSFGERTAGLA
 LLQVRGVNVVLVLEDPNHLDLAIEQLEQALASVDGVLVLTVDHRRMLDAVQTNRRWHVE
 AGEVREL

>RXN02280 TRANSLATE of: rxn02280.seq check: 171 from: 1 to: 1824
 MQESSRDNFQVLDLGGVVDLLSRHIYSGPRVYVRELLQNADVACTARSEQGEYEPSIRI
 RPVTKDRATFSLVDNGTGLTAQEARELLATVGRTSKRDEFGLQREGRLGGQFGLLSCFM
 VADEITMVSHAEGASAI RWTGHADCTFNLEILGDDATDVI PVGTTVHLT PRPDERTLLTE
 NSVVTIASNYGRYLPPIPIVQGEKNTTITSPVFAKDTQOHRLYAGRERLKTPTFDVID
 LTGPGIEGVAYVLEPAQAHPMSRRHSIYVNRMLVSDGPSTVLPNWAFFVECEINSTDLEP
 TASREALMDDTAFAATREHIGECIKSWLINLAMTKPHRVREFTAIDHLALRELCSQSDADL
 AETMLGLLTLETSRGRI SIGEITLSTEDVSLQLATLDDFRQNTIARPDTLIINGGY
 IHSDLARLPIVHYPLTVSTADLRESMDLMELPFLQDIEKAKALDAQVTESLKDFQIKG
 ATRVFPGADVPVVIIDSKAQASDRDNETQSATTDRWADILATVDNTLSRQTANI PQDQG
 LSALCLNWNNSLVRKLASTDDTAVVSRTRVRLVYQALLSSKRPLRVKERALLNDSLADLV
 SLSLSSDI

>RXN02325 TRANSLATE of: rxn02325.seq check: 7224 from: 1 to: 867
 MDHAHDSCSPTLRDRLEVTLQQLQPEKAVDLAAPHEGKVANITKVTSSNMEHTITQASKAK
 EVVVLIHGLSLPTFQDLEKDLHFQACNKGFRSVAIVDPDRSADVVARFRPKQIPVAVV
 KDGASIAEFNSLNKEPVAQWLDHFVSRETIPNEKEGDVDKQIDPRLWRAELVNAGDPERA
 ALQLEYQLPQDATVKRAHAASVSLARMSVADRGEDPIEKSRDPDDVNKALAAADMYVLW
 NQPDTLVALEIALALLPKPEARRIVELLNLFDPLDLVALEIRAQVGNAMS

>RXN02462 TRANSLATE of: rxn02462.seq check: 3189 from: 1 to: 1818
 MTXDVHYEVDERKTKVGVKEEGVEYVEDQLGIDNLYAPEHSQVLSYLNNAIKAQELFTRD
 KDYIVRNGEVMVDGFTGRVLAGRRYNEGMMQAEAKERVEIKENQTLATVTLQNYFRL
 YETKLAGMTGTATEAAELNQIYKLDVIAITPNRPNQREDTDLVYKTOEAKFAAVVDIIA
 ERTEKQCPVLVGTVSVERSEYLSQLLTRGKIKHNVLNAKHHEQEQAQVAGALGPAGAVTA
 TNMAGRGTDIVLGGNPEILLDIKLRERGLDPFEDEESYQEAWDALPAMKQRCERGDVK

REAGGLYVLGTERHERSRIDNQLGRSARQGDPGSTRFYLSMRDMLMVRFGVPTMENMMN
RLNVPDDVPIESKTVTNSIKGAQAQVENQNFEMRKNVLKYDEVMEQRKVIYERREILE
SADISRYIQNMIEETVSAYVDGATANGYVEDWDLKLNWALEALYDPSINWTDLVEGSEY
GKPGELSAEDRLTALVNDAAHAEYAKLEEAVSAITGGEAQIRNIERMVLMPIVDITKREHLY
EMDYLKEGIGLRAMAQRDPFLVEYQKEGGDMFMNGKDGIKEETVRQLFLSASSSSSKTRKS
LTNSEP

>RXN02543 TRANSLATE of: rxn02543.seq check: 6877 from: 1 to: 1854
MGRAGVIDLGTNSVVSLEGGEPVVIANAEGSRTTSPVFAKNGEVLVGQSAKNQAVT
NVDRITRSVKRHIGTDWSVAIDDKNYTSQEIARTLMKLRDAEAYLGEDVTDVAVITVPA
YFEDSQRAATKEAGQIAGLNVLRIVNEPTAAALAYGLEKEQEQTILVFDLGGGTFDVSL
LEIGDGVVEVRATSGDNLEGGDDWDQRIVDWLVEKQSSNGI DLTOKMMAQLRLREAAEK
AKIELSSSQSANINLPIYITVDADKNPLFDETLRAEFQRTIQDLLARTKTFPNQOVVKDA
GVSVEIDHVVVLGGSTRMPAVTELVKELTGGREPKNKGVNPDVEVAVGAALQAGVLRGEV
KDVLLLDVTPLSLGIETKGGVMTKLIERNTTIPTKRSETTTAEDNQPSVQIQVFGERE
IATANKLLGSFELGJIAPAPRGVPQIEVTFDIDANGIVHTAKDKGTGKENTITIQDGGG
LSQDEIDRMKIDAEHADEDKRRREEQEVNRNAESLVYQTRKFVEENSEKVSIEDLAKAVE
EAAKGVEEALKEGDELEATKAAVEKLNTESEQEMGKAIYEADAAAGATQADAGAEGAADNV
VDAEVVEDDAADNGEDKK

>RXN02736 TRANSLATE of: rxn02736.seq check: 2617 from: 1 to: 957
MIFELPDTTQQISKTLTRLRESGTQVTTGRVLTILVVTDSQSDVAATSEINSEAREHP
SRVILVVGDKTAENKVDAEVIRGGDAGASEMIIMHNGPVADKLQYVVTPLLLPDTPIV
AWMPGESPKNPSQDPIGRIARITDALYDRDDAEDRVENYHPGDTDMTWARLTQWRGL
VASSLDHPPHSEITSVRLTAGSGTSVDLAAGWLARRLKVVPVIREVTDAPTVPTDEFTGP
LLAIQRLEIVRTTGSIIITIYAHTLQVEMPESGNAPSIVAIGRRSESDCLSEELRHMDP
DLGYQHALLSGSSVKLETV

>RXN02832 TRANSLATE of: rxn02832.seq check: 1718 from: 1 to: 543
RGFVMDYTNQSLVAFFFKALTSYLKKNCLYVLVDPLYENLRNADGEIVKSYDNRAFRV
TMDKLGKYGHGPFVGYDSMSQIRWLSVLDDKDETLQDKEMDYQTRNNIKTKTYDIAQVKT
KTLTIDSTQTFDFLHMAEEKHGKFKRELPHYFEEMQKLYDDHAMLKAYIDINEYLKTLQ
L

>RXN02926 TRANSLATE of: rxn02926.seq check: 2083 from: 1 to: 1632
MTHETSVFGPADAQVAGDTKLKGRAKKEKTPSSMTPEQQKQVWVLSALMVAMMASLD
QMI FGTALPTIVGELGGVDHMMWVITAYLLAETIMLP IYGLGLDLVGRKGLFIALGLIFL
IGSVIIGLAGNMTWLIVGRAVQIGGGGLMILSQAIADVVPARERGRYMGVGGVFGLS
AVLGPLLGGWFTTEGPGWRWAFWMNIPLGI IAGVAIYFLDIPKKSVKFRWMDYLGTFMMIV
AATSLILPTTWGSGQYENSODPI IIGLIITIVAAALVVVELRAKDLPLVMSFFQNRNFT
LTTIAGLILGIAMGFIIGYLPYLMQVHGINATEAGYMLIPMMVGMGTSIMWTGIRISNT
GKYKLFPIGGMVTVFVALIFFARMEVSTTLWQIGIYFLVLGVGLCLAMQVLVILVQNTLP
TAVGVSATAVNNFFRQIGSSLSGALVGGMFVGNLGLTMEERMPAAMAQLSPEEQAMAAQ
GGLDSDNELTPAIVNQLPTALHDAFAGSYNDALIPVYVMPLIGIALLLLLTKQEKLR
TTTD

>RXN02949 TRANSLATE of: rxn02949.seq check: 1467 from: 1 to: 333
VSDENQSGVGSTSRPTGKRLSGASTTSSSYEAKQVSTQKSSGSDSKPGGGVISFLPE
VVGVEVRKIWPTARQMVTYTLVVLGLFVLIVLTALVSGVDPLAGLVGEKILTP

>RXN02964 TRANSLATE of: rxn02964.seq check: 1405 from: 1 to: 1218
VSVAEEGKLTPTPTFMGMFANLFQFLVYFLITTMALYAIKEFQASEVEAGFASSIVIG
AVFSRFFSGYI IDRFRGRKIVLISVLVTTIACALYLPIESLPLLYANRFLHGVGYAFAAT
ATAMVMQQLIPASRRSEGTGYLALGTTVSAAALPALALFVLGTFDYDMLFIVLATSVIS
LIAVVMYFKTSDPEPSGEPAKFSFKSINMKPIIPIGIFILLICFAYSGLVIYINAFEE
RDLITAGLFFIAYAVSMFVMSRFLGKLQDRRGDNVVIYFGLFFVVISLTILSFATSNWH
VVLGVIAGLGYGTIMPVQSIAGVVDKTEFTGTAFTSTFLFVLDLGGFGPGIILGAVSAA
IGFGPMYAAAGVGIAGIFYLFTHARTDRAKNGFVKHPEPVALLV

00603200-062300

>RXN03022 TRANSLATE of: rxn03022.seq check: 1371 from: 1 to: 447
VIIITAGILVATATALLMITAVSESTYIVISLAGFSLYGLGLGLFATPVTDLTALGLPKDR
TGAGAGVFKMSSSLGAALGIAISTSVFLALRDGTSINSNDVALAGTVSLGINVVFATATI
TAAVLIKPAAGKVSQTSITLPEPAIAVKI

>RXN03038 TRANSLATE of: rxn03038.seq check: 812 from: 1 to: 726
MHSKEELTVRKGLSRVLSVAVASSIGFGTVLTGTGIAAQAQSAFDYGMDFNMNYPIDDI
KDRPEGLSNLPYFGSKLTSWGSSYATASSGVVTSALPQYTDPRYPLGKDDLPKATIIMEP
EVLARLERFVVGDDRIQINAYSPSMGRTIPLVWVVPEDNTVPGPTVYALGGGDDGGGG
QNWVTRTDLEELTSNNINLIMFMLGSFSFYSDWARESQSMGCAQQWETLLMHELPEPLV
AA

>RXN03039 TRANSLATE of: rxn03039.seq check: 1469 from: 1 to: 630
ALPQYTDPRYPLGKDDLPKATIIMEPEALARLERFVVGDDRIQINAYSPSMGRTIPLV
WVVPEDNTVPGPTVYALGGGDDGGGGQNWVTRTDLEELTSNNINLIMFMLGSFSFYADW
AGESESMGGAQQWETFLMHELPEPLEAAGDQGRSIVGMSMSGGSVLNFATHDPENFYSS
VGSFSGCAETNSWMGRWRHSHCLQRQCRA

>RXN03040 TRANSLATE of: rxn03040.seq check: 6898 from: 1 to: 309
MXSGDNAPIDDEAFKNRVLVGFIEIAMSNTCTHNLKAATDQMGININYDFRPTGTAWD
YWNELHRFFEDFLMMQGFGLDGGGPIPIYNPENGVTSSSSXRTVF

>RXN03042 TRANSLATE of: rxn03042.seq check: 1569 from: 1 to: 606
LVLAFLVLLVFRSIVWPLIAALGFLSVLALTFGATVAIFQEGAFGIIDDPQLLSFLPI
MLIGLVFLGLAMDYQIFLVTRMREGFTKGKTAGNATSNCFKHARVVVTAALIMVSVAFA
IAQDMAFIKTMGFALAVAVFFDAFVVRMMIIPATMFLDDKAWWLKPLWDLKILPNVDVEG
EGLSELHEARTEELKENVGVGA

>RXN03051 TRANSLATE of: rxn03051.seq check: 1794 from: 1 to: 735
MRSOVIELPEGVSKADQLEVAEARLNEGARIIMATTGCEVMMWPTGFSVCGRIIDTYRQV
GGQLSWLGPSPKSNELTNPDGVGKRSEFFGGAIYVHPDGTAYAVLTDGLQWGTNLNWSGP
LGYPTSGPMDTNYPLTQRQTFQGGDNYYNPLTGGAVWGIQORYEELGGSNAHIGIPITN
ELPSTGEYFYNNFNSNGTISWRNDRQTRFMYLATQRVWDALGRETGRIGFPEADETPEVSG
LFHVA

>RXN03054 TRANSLATE of: rxn03054.seq check: 8742 from: 1 to: 1581
MKLFSKAAGVIAAALLVAGGIAPVAQQQASQVVTPEDDQAYVQQFHHGENTPPVVDGVGG
YTEQEIIEIHEAIRAQESGAPNEELIPGEMWSDKVELPVTIDKAAADEAEIAIAQQQSQ
PQTRGLAAACQTFWSPSPHQVCGAILERYIQGAQFGWMLFPSEGGTLNPDGGQGYRQRF
MNGFYVWHPTGAHAVNNYSAQVWERNWESGWMGYPTGGEVPVNGSNPIDGELSGWVQT
FQGGVVRYSVPLDGFQVASINGLILDKWLELGGPDSDLGFPIADEAVTADGVGRFSVFQN
GVVYWHPHGAHPILGNISYIWRREEGASGEFGYPIGDPPEKYTENMANQVFEKGLAANL
YPNPLEAIEFLPFANLEEAIEYFENGLSNRSRVANSNLAKKDIQCSQSNAINHVRTKS
DGVGIRVPKIGFKARMDCLPGTVSDVVGYGWIYYDWGRWAQAAAYQQFGNRRNSVVQT
NLEAGCSGKNTLFWGTSYFQVTEYEQPFYQGSATNAYLEPCTIDRS

>RXN03064 TRANSLATE of: rxn03064.seq check: 5850 from: 1 to: 1332
MLMNETTALVALPSIMADFDIEANTAQWLLTGFMLTMAVVLPATGWMLEFRTTSRVFI
TVVFLITGVTAALSPTFAMILAAARVAQAICTAVIMPLMLTAMTVVPPERARGAVMLIAV
VMAGVFPALGPSVAGFVLSLSSWHAFVWMVPLVFVAGSLIGTLRLTNVSEPKTPLDVISF
LISAVAFGGVLVYALSSIGIILEGDRSALVVLAVGIITLVVFWQIAMGQKDKALLDLRP
LAIREYTIPLVLLTLFGALLGVMMNTLFLYLGQSLMVTALVAGLVLLFGGLLEGLVSFV
GRIYDRHGPRGLVIGMSLVVISLFASTVDEAFANVWFIIGVHIVFSIGLALLFTPLMTV
ALASVPDNMYGHGSAILNTLQQLAGAAAGTAVMIAYVSTVSNNALIDGATQQTALADGANS
AFFASACVAVFALINGFVFKRPAR

>RXN03075 TRANSLATE of: rxn03075.seq check: 8649 from: 1 to: 726

00630220-2023060

VAKFLYKLGSTAYQKKWFFLAWVLVILIGITTLAGLYAKPTSSSFISIPGLDSVTTMEKMQ
ERFPGSDDATSAPTGSVVIQAEKGKTLTDPVGAEVNQMLDEVRAATGVLKDADSVVDPVL
AAQQAQVAAQMPALAEAGQVPAEKIAADIESISPLSADETGTIISMTFDADSAMDISAEDRE
KVTNILDYDDGDLTVVYNGNVFGAAATSLDMTSELIGLLVAAVVLIVTFGFSFIAAGMPL
IS

>RXN03119 TRANSLATE of: rxn03119.seq check: 3185 from: 1 to: 132
MAVYELPELOYADALEPHIVAEIMELDQSKDHATYVAGANAAL

>RXN03120 TRANSLATE of: rxn03120.seq check: 209 from: 1 to: 126
MLDMWEHAFYLYQMVNKADYVKAUVNVFNWDDARARFAAASK

>RXN03123 TRANSLATE of: rxn03123.seq check: 5888 from: 1 to: 438
VGDALRGGRGPEVMRYPGIIPFAIPDPAPRGFLGDLTSTYPAICSILETLDGEIIPATAYL
IAHDPDYTFDFPQGEHITAQWISNEQSFIDHIAADTYDTFYTWIGAESSETRAACKHKLQ
THAGMPKTHMNAQGYWNKGRAMGKSN

>RXN03124 TRANSLATE of: rxn03124.seq check: 3878 from: 1 to: 960
MTPTLASMIGLAVGIDYALFIVSRFRNELISQGTANDLEPKELAEIRLTMPLAARAHAMG
MAVGTAGSAVVFACTTVLIALVALSIINIPFLTVMIAIAAITVAIVLVALSFLPALLGL
LGTRIFAARVPGPKVPDPDEKPTMGLKVVRLVRKMPVAYLLVGVVLLGAIAPATNMRL
AMPTDGTSTLGTAPRTGYDMTADAFGPGRNAPMIALIDATDVPEERPLVFGQAVEQFLN
TDGVKNAQITQTTENFDIAQILLPQNLMRMSAPLRLSLQFLVQMLRPSLMTPARMALLA
SQPFTMTSLLASATGSWFLTF

>RXN03125 TRANSLATE of: rxn03125.seq check: 4701 from: 1 to: 171
LVLAFLVLLLVRFSIWVPLIAALGFGLSVLATFGATVAIFQEGAFGIIDDPQLLFCF

>RXN03142 TRANSLATE of: rxn03142.seq check: 9643 from: 1 to: 1143
VFILGWLVLNLTQVLSFYFLITVMALYAMESFAVSEAAVGAASFSVIGATVARVFAWTS
DRFGKQKILLIFVGLAEVASLFIYIPASLPALVAVRFVHGFSYSLASTAVMALVQSIVIPA
SRRAEGTGYFALGSGTLTAFAFGPAIALFVIDDFNYNTLFWITATTSTSVFGLILTVLRKPEF
IKNAEHGRVVKPVWSIKTVVHPSVMLIGFFMLAVGLAYAGVITFLNGFAQDPTGLTAGAGLF
FIAYAVAMLVMRFFFLGRIQDKHGDNPVIYFGLISFALALGLMALATEDWHIVLALAGALTGL
GYGTIMPAQAIAVDSVPSTQVSGISITLFLFTDIGLGLPILLGGLVAATGYNVMYAAL
AAVIVVAGTVLVVALGRKASH

>RXN03151 TRANSLATE of: rxn03151.seq check: 6293 from: 1 to: 486
VLSHIIDVLADPIDGTPLVGAEDFSRLVSESGHSYDVBARQQYVTLAGGAGLRYSGDDAQM
ADRETFLVSGGHFAPFVEAVTEHVQDVVDQAGLSDDAQPVVCEIGAGTGYYLSHTLDSVA
GSRGIGIDVSVHAAKRLAKCHPRVGAIVIANAWARLPIDNNS

RXS00568 translate of: RXS00568.seq check: 2511 from: 1 to: 1347
VKSSVEKLSDRSKITVEVPFSELKPEIDQAYALAQQVQIPGFRKGKAPRQLIDAREGRGAVLEQVNV
DMLPNRYAQAEIAEGIKAIGQPNVEVTKIEDNELVEFVAEVDVREPEFELPKFEDITVEVPAIKADEEAI
EAELETLRAREFTLKDHNHKLKKGFEVTTINITASIDGKIEEATTEGLSYEIGSDDLDGLDKALIGAK
KDETVEFTVSELANGHEHKGKQAEISVEITATKQRELPELDDEFAQLASEFTDTEELRESTVSDVEAKQKN
EQAAAIIRDEVILAALGEADFALPQSVIQVDEQAHSQHLQGLGELAHDAAALNSLLEAQGTTREEFDKKNVE
DAEKAVRTQLFDLTSEVEEPEVSQQELTDHILFTAQSYGMDPNQFIGQLQSQSQIANLFSVDRRGKAL
AQAIRCVNVKDSSEGNIDFKEYFGEVEVAETESEA

RXS01027 translate of: RXS01027.seq check: 2562 from: 1 to: 1008

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MANKNNKPHEVDKQDSAMLINGRLQQIPARPTEEFTRPTLAAGAVLWRGDITNPDSIEVAVIHRPHYD
DWSLAKKVDPGESIPTTAAREILEETGYDIRLGKLGKVTYPVLDRTKVVYWTQAQVLGGGFVFNDEV
DEIRWLSVDEACELLISYQVDEVLAKAAKRFTPTSTRVLYVRHAHAHGRQWGGDDNKRPLDKKGRQ
AEMLVFMLLPFKPTAIYSAPVDRQCATALPLADELGLDVSVNRFLGDDAWETDPEACKKRFDTVVAQGG
VPMIVGQGDIIPEMIKWFSENGTLPIDEKIKAKKGSVWVLSFHDGVFTGADYLASSLPVK

RXS01528 translate of: RXS01528.seq check: 2639 from: 1 to: 528
VNQAWQQSRVLTSDETSAGGLVVSGLAEAVNANNEVDLSKIYVALIGRLDRGRLLNSMPKGHVEPGED
KAATAEREVWEETGIHGEVFTELGVIDYWFVSEGRKIHTVHHLLRYVDGDLNDEDPEVTEVAMIPAN
QIEHLAFADERKLARQAHDLLEFALKEKAEGRSTPR

RXS01716 translate of: RXS01716.seq check: 2732 from: 1 to: 486
EVTPEGKETRENTIVRLGKGVDTATQGLDPEAIERTVALENYVELMETHGVEAVRMVATSFATRDASN
RDEFFSMTROLLSKIRPGYQAEVISGEEALLSPRGAIVDLPEAQGFPCVIDLGGGGSTEFIVGTYDGEI
LGSHTQMGCVRLTERIMRSDPPD

RXS01835 translate of: RXS01835.seq check: 2495 from: 1 to: 531
MNTAAWAHRRHVRRGGGIPYVSHLYSVMYLLASVTNDEVDVLIAGLLHDTLEDVPEEYNSAQLEADFGPR
VRELVEELTKQPLKSWKARADAYLHLHAGASLEAVLISTADKLHNLMSILDDLEIHGEDLWQRFNAGK
EQQVWYSEVYQISLQRLGFNELNKQLGLCVKLLKQSA

RXS02497 translate of: RXS02497.seq check: 3482 from: 1 to: 927
VRLGLVDVGSNTVHLVAVDARPGGHPTPMSNWRTPRLVELLDSDGAISEKINKLTSVAGEAADLAKT
LGCaelMFFATSAVRSATNSEAVLDHVEKETGVRLSILSGEDEARQTFVARRWYGSAGRITNLDIGG
GSLELSSGTDESPLAFSLDLGACRLTHNWFDTDPARKKINLLRDYIDAEAEAPARQMTLGPRLAV
GTSKTFRTLRALTGAAPSSAGPHVTRTLTAPGLRLQIAFISRMATAADRAELEGISSDRSHQIVAGALVA
EAAMRALDIDKVEICFPWALREGVILTRIDKGLE

RXS02972 translate of: RXS02979.seq check: from: 1 to: 411
VGIAAATVAGAIGGVLAIVPISALTPVGCAGTPTTISATVGGLGSTAAAAIHLAL
APAAALAVVTATISGSSSAGASAPVVAAGAAVGGGSVVGAIALASLGLAGVATIIISGLAILA
GLILGLVGAASLLL

RXS02979 translate of: RXS02979.seq check: 3131 from: 1 to: 234
MTAPNTLKQTTLRSDFCPCSPCVSKIKENKLNGLDGVNAEVKFSSGRILVDHDPKVSIDKLVAVAEV
GYTAKPSAI

RXS02987 translate of: RXS02987.seq check: 9782 from: 1 to: 234
MTAPATLKNNTLRSDFTCPSCVAKIKENKLNGLDGVNAEVKFSSGRILITHDPQKVSVRDLTVATAEV
GYTAKPSAI

RXS03095 translate of: RXS03095.seq check: 5530 from: 1 to: 369
MNAKKMKCMNPDSQYVELAVEVFGLLADATRVRIILALRNSGELSVMHADIIVKSPAAVVSQHLARLR
MARIVSTRQEGQVRVFKLTNEHASQLVSDAIFQAEHTIADGQTPPHHRREREQS

RXS03217 translate of: RXS03217.seq check: 67 from: 1 to: 201
MAQGTVVKWFNGEKGFGFIAPNDGSADLFVHYSEIQSGGRNLEENQPVFEVGEAGKGPQAAQVRL

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APPENDIX A: DNA SEQUENCES

>RXA00062-upstream
CTTCAACATAGCGCTTGGGGCTGACTTTTAAACAGGTACCAGTAGTACCGGCATAAGCGA
TCACGTGTGCGCTTTTCTGTGCTGCCATCAAAATTAGTCAC

>RXA00062
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GTGACAGATTCTCACACATTAGTCTTCGGCGCACTTCTTCTGCTGGGAGCTCGTGCCGGT
GATATCTTCGGCCGAAAGAAAGTGCTACATTGGTCTCGCGTTGTTTGGCGCTTCATCG
TTGGCAATTGCGCTTCTCCTCAATGCTGCGGTCTCATTTGGAGCACGCGTAGTTCAAGGC
GCGGAGCTCGGATTATCGCTCCAGCGACACTTGGCTTGAATCTAGTGTGTTTCCCGGAA
GGCCAGCTCGCTTCGTGCTACCTCTGCTTATGGTGTGTTGCCGCACTCGGTGTGGCA
GCAGGCTAGTGATCGGCGGCGTATTTGCTGATCTTTTGTGCGGCACTCGGCTTCTTT
ATCAACGTCCCATCGCGCAGTGTGGCTACATAGTGCACAAAGCCATTCCCGCAACC
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GCGGTGCTCTACGCAATTGTCCGACGCGCGATTACAGCTGGACAGATCCGTTTGTGTTG
ATTTCCCTCGTGTGGGCATCGCAGTGTTCATCTGGTTCCTGCGCCATGAATCCTCAGCC
AAGAACCACTTCTGCCCTGGGGCTCTTTAAACACCGAGGCGAAACACCACTTTGGCC
AGCGCTTCTTCTGGTTGGCTCCGTGATGTCTTCTTCTTGGCCACCCAGCTGTTC
CAGGACACCATCGGAATGAATGCTCTCCAGGACGGCTTGGCTTCATGCCGCTATCTCTG
CTGCAAGTTGCCAGCGCGCGATGGTGCCACGGCTTTCGCCAGCAGGCGTATCTGATTC
ATGCTCACCGTCTATCGGTTTCGCCATCATGGTCTATCGGCATCGCAGGCTTCGCAATTTGT
CCAACACAGATGATCGCGCTGATCCTACCAATAGTTTGGTGGGATTGGCGAAGGCTTC
GCTTTCGGACCAATGACAGCTCTGGCAGTTCAAGGTGACCCGAAGGACCAATCCGGCGCC
GTTTCTGGCGTGGTGAATTCCTTACCAAAATCGCGGCACTTCGGTTTGGGTGTGTT
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>RXA00605-downstream
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>RXA00648-upstream
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>RXA01054-upstream

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06603208-062300

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000290-20200900

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00603200-062300

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>RXN03054-upstream

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>RXN03054

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>RXN03064

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0060290-062300

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>RXN03142
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>RXN03142-downstream
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>RXN03151
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>RXS00568 - 5'-Region
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>RXS00568 - coding Region
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>RXS00568 - 3'-Region
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>RXS01027 - 5'-Region
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>RXS01027 - coding Region
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>RXS01027 - 3'-Region
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>RXS01528 - 5'-Region
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>RXS01528 - coding Region
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>RXS01528 - 3'-Region
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>RXS01716 - coding Region
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>RXS01716 - 3'-Region
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>RXS01835 - 5'-Region
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>RXS01835 - coding Region
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>RXS01835 - 3'-Region
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>RXS02497 - 5'-Region
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>RXS02497 - coding Region
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>RXS02497 - 3'-Region
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>RXS02972 - 5'-Region
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>RXS02972 - coding region
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GAC ATC CTC GAC GGC CTC ATC CTT GGC CTG GTA GAA GCC GAC TCT TTG AAG
AAA

>RXS02972 - 3'-Region
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>RXS02979 - 5'-Region
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>RXS02979 - coding Region
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>RXS02979 - 3'-Region
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>RXS02987 - 5'-Region

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>RXS02987 - coding Region
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>RXS02987 - 3'-Region
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>RXS03095 - 5'-Region
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>RXS03095 - coding Region
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TTCGGACTCTCGCGGACGCCACTCGAGTTCCGATCATCTTTGGCACTTCGAAACAGTTGGTGAACCTTCC
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CACCACCGAGAACGAGAACATCA

>RXS03095 - 3'-Region
TGACCACCCACAGTCACCAAGAA

>RXS03217 - 5'-Region
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>RXS03217 - coding Region
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>RXS03217 - 3'-Region
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00603208.062300

cacagtgggtt gaccactggc

20

09603209.062300